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(54) **GENE SIGNATURE.**

(57) A 3'-directed cDNA library which accurately reflects the abundance ration of mRNA in a cell has been prepared from various human tissues, and sequencing of the cDNAs contained in the library has be conducted to examine the incidence of each cDNA in each tissue. As each cDNA has expression information with each tissue corresponding to the mRNA concentration, these cDNAs are usable as a probe or primer for detecting cell anomaly or discriminating cells. The cloned gene can produce porteins utilizable as a medicine or the like.

EP 0 679 716 A1

[illegible]

	A	B	C	E	G	I	K	M	O	Q	S	U	W	Y	AA	AC	AE	AG	AI	AK	AM	AO	AS	AL	AW	AY	BA	BC	BE	BF	BGBH	BI	BK		
94	00105	00093	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
95	00106	00094	8	2	1	1	0	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0							
96	00107	00095	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0								
97	00108	00096	31	2	3	0	0	1	0	2	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3X63237	94.8	384	1	154	532	
98	00109	00097	5	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
99	00110	00098	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0							
100	00111	00099	38	7	0	0	1	9	13	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.373	1	983	1352		
101	00113	00100	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
102	00114	00101	38	1	1	5	0	1	0	0	3	0	1	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
103	00115	00102	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.2	383	1	1551	1918	
104	00116	00103	17	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.6	362	1	840	1200	
105	00117	00104	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
106	00118	00105	7	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
107	00119	00106	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
108	00120	00107	5	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
109	00121	00108	4	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
110	00122	00109	4	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
111	00123	00110	14	2	0	0	0	2	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8	336	1	144	479
112	00124	00111	6	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
113	00125	00112	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
114	00127	00113	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
115	00128	00114	6	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
116	00129	00115	11	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.348	1	4238	4586	
117	00130	00116	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.6	348	1	168	518	
118	00131	00117	6	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
119	00132	00118	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
120	00133	00119	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
121	00134	00120	24	1	0	0	1	0	1	1	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
122	00135	00121	81	5	4	0	0	14	2	4	2	0	2	0	4	1	1	0	3	5	14	1	12	1	2	4	0	0	0	99.1	339	1	2205	2543	
123	00136	00122	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.7	307	1	416	723	
124	00137	00123	10	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0					
125	00138	00124	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4	313	1	767	1078	
126	00139	00125	8	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.4	335	1	1698	2029	
127	00140	00126	13	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
128	00141	00127	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						
129	00142	00128	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0						

Table 4

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: CHUGAI PHARMACEUTICAL CO., LTD.
(B) STREET: 41-8, Takada 3-chrome, Toshima-ku
(C) CITY: Tokyo
(E) COUNTRY: JAPAN
(F) ZIP: 171

(ii) TITLE OF INVENTION: GENE SIGNATURE

(iii) NUMBER OF SEQUENCES: 7848

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.5 in., DS, 1.44 MB
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/ MS-DOS
(D) SOFTWARE: MS-DOS

(v) CURRENT APPLICATION DATA

(A) APPLICATION NUMBER: EP 95900295.7

(vi) PRIOR APPLICATION DATA

(A) APPLICATION NUMBER: PCT/JP94/01916
(B) FILING DATE: 11. November 1994

SEQ ID NO:111

SEQUENCE LENGTH:375

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00124

SEQUENCE DESCRIPTION:

GATCCTACCT ATCAAGCACT AAAAAGTTGA ACCATTATAC TTTATATCTG TAATGATACT 60
GATTATGAAA TGTCCCTCA AACTCATTGC AGCAGATAAC TTTTGTGAGT CATTGACTTC 120
ATTTTATATT TAAAAAATTA TGGAATATCA TCTGTCATTA TATTCTANTT AANGTTGTGC 180
ATAATGCTTT GGAANAATGG GTCTTTTATA GGAAAAAACC TGGGATAACT GATTTCATG 240
GCTTTCAAAG CTNAAATATN TAATATACTA AACCANCTCT AATATTGCTT CTTGTGTTTT 300
ACTGTCAGNT TAANTTACAG CTTTTATGGG TGGTTAACTT TTCGTNCATT TTCAAAAAAN 360
CCNGGGGNNN NNNNN 375

SEQ ID NO:112

SEQUENCE LENGTH:356

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00125

SEQUENCE DESCRIPTION:

GATCTCTGTT TTGTTGTTGA AAATTCATTT GTATACTTTT GTTTTNACTT AGGACTTCAT 60
GTTTTTTNAA AGCACTGGCA GCCAGGAACA AAAATCAGGA GTGTGGTAGT GGATTAGTGA 120
AAGTCTCCTC AGGAAATCTG AAGTCTGTAT ATTGATTGAN ACTATCTAAN CTCATACCTG 180
TATGANTTAA GCTGTAAGGC CTGTAGCTCT GGTGTGTATAC TTTTCCTTTT CAAATTATAG 240
TTTATCTNCT GTATACTGA TTTATAAAGG TTTTGTGACA TTTNTNAATA CTCATTGTCA 300
ATTTGAGAAA AAGGACATAT GAGTTTTTNC ATTTATTAAT GNAACTNCCT TTGAAA 356

SEQ ID NO:113

SEQUENCE LENGTH:351

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00127

SEQUENCE DESCRIPTION:

GATCACATTA TNATAAATAA ATGAAAAAAT GATTTAATCT GTAATAAACT GGTTTATTGT 60
GCAGTGACTG TAATATACTA GAGTTATAAT AAATTGTTTA CTCTGCCTCA CCAAACACAT 120
GCTAGGATAT AACCCCCAAA ATAAGTATTT AACTTTGCAT TAGGTATAAA GGAGACTGGG 180
TGCTATAATN AGATTATTTT GAGGCAGACA GAGAGCTGTT ATCCTAACTG ATTTAGTATG 240
TTCTGTAATT GAGAAAATGT TCACCAAATN ATACTTTTTA GTGATTTACA TGTACATTTT 300
ATAGGGGACA TGTTCGTGT ATAGCGAATA AATAACTTTT ATAGTATCAC N 351

SEQ ID NO:114

SEQUENCE LENGTH:352

SEQUENCE TYPE:nucleic acid

TOPOLOGY:linear

CLONE:HUMGS00128

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SEQ ID NO:7844
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATCCTTATA CAGGCTCAGT TTTGTCT 37

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SEQ ID NO:7845
SEQUENCE LENGTH:37
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTCGCTCGCC CATGTATAGG GACAGCATTT CTGAGAG 37

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SEQ ID NO:7846
SEQUENCE LENGTH:38
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CTGGTTCGGC CCACCTCTGA AGGTTCCAGA ATCGATAG 38

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SEQ ID NO:7847
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
CCAGGGTTTT CCCAGTCACG AC 22

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SEQ ID NO:7848
SEQUENCE LENGTH:22
SEQUENCE TYPE:nucleic acid
STRANDEDNESS:single
TOPOLOGY:linear
SEQUENCE DESCRIPTION:
TCACACAGGA AACAGCTATG AC 22

50 Claims

- 55
1. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

2. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
3. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto comprising any of the base sequences listed under SEQ ID NO 1-7837 and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
4. A purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
5. A DNA probe consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.
6. A DNA primer consisting of a purified single-stranded DNA, a purified single-stranded DNA complementary thereto, or a purified double-stranded DNA consisting of said single strands, containing all or a portion of a single-stranded DNA or a single-stranded DNA complementary thereto, wherein said single-stranded DNA is complementary to a human mRNA containing any of the base sequences listed under SEQ ID NO 1-7837 (wherein T is read as U) or any portion thereof at its 3' region, and hybridizing specifically to a particular site of human genomic DNA, human cDNA or human mRNA.

Fig. 2

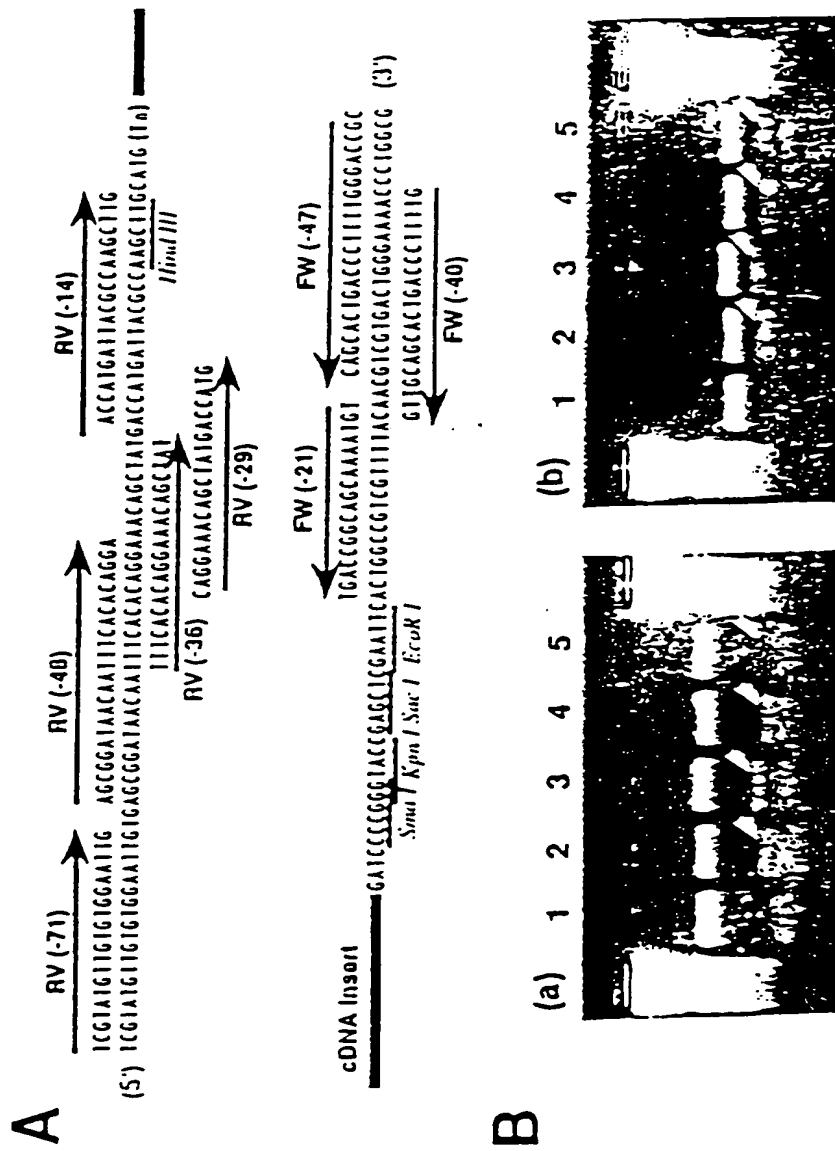


Fig. 3

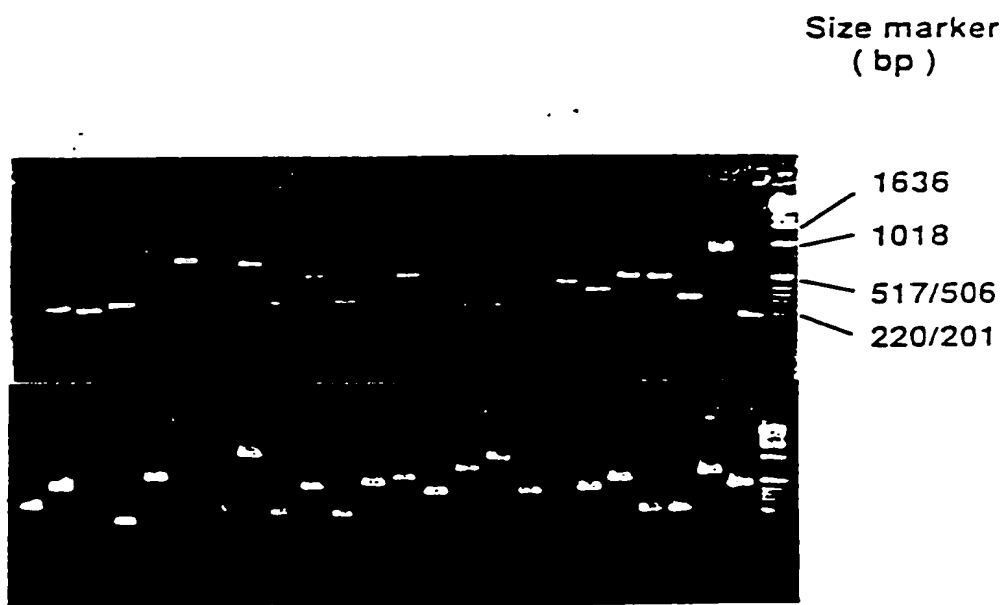


Fig. 4

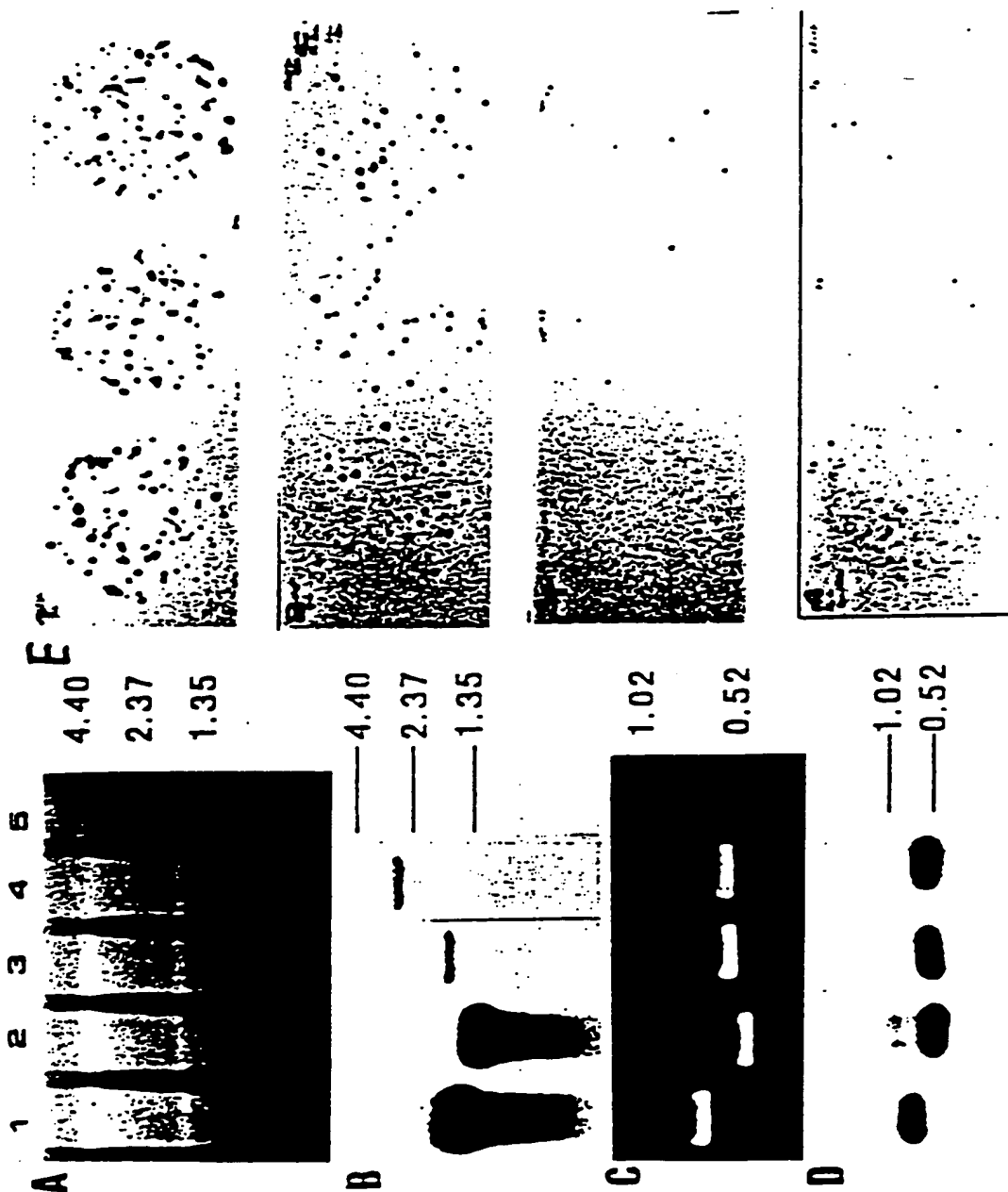


Fig. 4

F

probe No.	1	2	3	4
gene	Elongation factor 1- α	α 1-andrypsin	HnRNP core protein A1	Inter- α -trypsin inhibitor
(a) Band intensity of Northern blot(cpm)	687	423	10	15
(b) Band intensity of control blot(cpm)	133	177	100	127
(c) Normalized signal(a)/(b) $\times 10$	52	24	1	1.2
(d) Positive signals on colony blot	307	119	7	9
(e) Relative representation	44	17	1	1.3

Fig. 5

Appearance frequencies of various cDNAs in the 3'-directed HepG2 cDNA library

Group	Clone	Gene	A in 902 (%)	B "in 0,000 (%)"	C "in 26,400 (%)"
I	a15	Elongation factor - 1A α	22 (2.2)	307 (3.5)	NT
	c321	Translationally restricted tumor protein	12 (1.2)	89 (1.0)	NT
	ib030	α -1-antitrypsin	0 (0.0)	119 (1.4)	NT
	hm01b02	Light chain of ferritin	6 (0.6)	62 (0.7)	NT
	c13a04	NADP(H) Menadiolone oxidoreductase	4 (0.4)	27 (0.3)	NT
	hm02d02	Ribosomal protein S11	3 (0.3)	29 (0.3)	NT
	ib042	Human RNP core protein A1	2 (0.2)	7 (0.1)	NT
	s155	unknown	1	2	5 (0.02)
II	s159	unknown	1	2	4 (0.02)
	s639	unknown	1	1	3 (0.01)
	s635	unknown	1	0	2 (0.01)
	s170	unknown	1	0	1 (0.004)
	s154	unknown	1	0	1 (0.004)
	s167	unknown	1	0	1 (0.004)
	s645	unknown	1	0	1 (0.004)
	s647	unknown	1	0	0 (<0.004)
	s632	unknown	1	0	0 (<0.004)
	s632	unknown	1	0	0 (<0.004)

GS	CII	Chromosomal position	Sequences of primers		AT	HO	HE	HO	CO	G	T
			Sense	Anti-sense							
91000708	pin2366	1	CAGAGCCCAAGTACAACTAT	AAGTTATGTGGGGTCAG	48	114	115	104	110	1	2
91001026	pin2444	1	AATGGACAGTTACACITGA	CCAGCTTCCTTGACTTGAGA	48	83	81	>200	>200	1	1
91001075	pin0883	1	TGGACTGTGGATACCTATCT	ACAGTACCCTGGAATGCT	48	124	124	103	107	4	4
91001087	pin1772	1	GTACCTCTCAAGCCATAGCAC	ACATCTTCAGCCACACACTT	50	104	104	180	>200	6	6
91001094	pin0347	1	GCCTCTAACACAGGAACTC	TAATTCCTACCTCCGTAACT	51	114	116	>200	200	1	1
91001116	pin1771	1	GGGTTTCAATAGGTGTAGACC	GCCTCAATCTGTCAAACTG	49	95	95	78	107	1	1
91001191	pin0609	1	TTCGTGGATTGAACITTTTG	GGCTGAACATTCAGCTCTTG	47	97	97	200	200	1	1
91001200	pin1351	1	TAAAGAGACCTTATGGAGACC	AATACTTGTGTAGTCACTTAC	47	97	98	-	-	1	1
91001316	pin0982	1	TCAGGTCTGCTGGAGGATG	AATCACAGCACAGTATTGG	53	120	122	>200	>200	1	1
91001416	pin1518	1	AAGGTGTACAGGATATTGCAGA	TGCAATAGCCCAATCTCAT	47	130	125	>200	>200	1	1
91001464	pin1439	1	CCAAAGACCTCCGTTGAACA	TTTGGAGAGCCATAGACAG	51	100	100	>200	-	1	1
91001468	pin0427	1	TACTCAGTGGMAAGATAAAC	CAGTGGACCAATTTCTTA	40	98	98	-	-	2	2
91001521	pin2785	1	CCCAATCAATTTGTTAAATG	TTTGAATCAGAGACATGAAGTT	43	102,175	100	>200	>200	1	1
91001554	pin2291	1	CCAGAGAGTCAAGGCAITG	GGTACAAAGTGCAATGACT	46	57	57	78	155	1	1
91001572	pin2006	1	CCAACTGTCTCTAGCAGCTG	AACTTTATTCAGCTTCIT	44	58	55	>200	>200	4	4
91001603	pin1350	2	CATGATACCTCTCTGCTGTA	AMACAGTAGTCCCAAGCAIT	46	84	109	-	-	1	1
91001606	pin1730	2	AGCTGAATGTGGCATGCT	CCCGTTATGTGACATGCT	48	119	119	93	115	1	1
91001601	pin0931	2	AAAGCAATACAAATACCAA	TTCATATGTTTAAACAGTA	40	90	90	-	-	1	1
91001650	pin0825	2	TAAGTACACAGATGAATAG	TATGTAAATAGCAGGTAA	45	88	88	-	-	1	1
91001712	pin2010	2	CCAGATGGAAAGGGAAGTCT	CTGGAATATGGAGAATCAACAG	47	125	125	150	>200	1	1
91001752	pin0935	2	TGAGTTTGTCTCTAATAA	GGAAATATCGCTTCAGTIG	43	103	103	-	-	1	1
91001768	pin2093	2	AGTCCTCTTGGCTCCTCAT	TATGTCAGTGGCTTTATIG	52	137	137	>200	-	1	1
91001835	pin2435	2	TTTGTACTACGTAGAGTACTT	ATCCGTGCCACACATAGTGA	45	105	108	-	-	1	2
91001871	pin1671	2	TATTAGGAGTCATTATCTGTG	AGTCCCATCTCCCAATG	45	67	65	>200	>200	1	2
91001913	pin1245	2	TTCCTTCCCGTCTAAGT	ATGTACAATTTGGTATGTAGG	45	75	75	170	190	1	1
91001935	pin1246	2	ATCTACTGTTTGTGAAGTG	ACTGATTTGGTCCCATCTG	44	68	67	-	-	1	1
91000875	pin0448	3	CGAACATTTCCACCTCATA	ATGATTTATTAGCCAGGA	43	68	65	-	-	3	6
91001001	pin1758	3	TCTGGCTCTTTGGTGTGGA	GGCCCACTGAGTACAAATGTC	51	115	115	-	-	1	1
91001218	pin2434	3	AAAGAAAGCACACTGCCTAA	ATGTATAGACAATCCAAAG	42	90	90	-	-	1	1
91001219	pin0668	3	GTAGTCTCCGCGCTTTAGC	AAGGATTTGATTTCTACAT	43	77	77	-	-	1	1
91001277	pin1729	3	GGTCTGTTTATTTCACAT	AMCAAGAGGATGGTTCAGA	43	75	75	155	>200	1	1
91001306	pin1022	3	GATCCTTGGTGTAGTTCAGTC	CTGCAATACAGGGAATCAT	46	83	83	160	140	1	1
91001418	pin2209	3	ACCCAGTCCCAATCCAGT	ACACTCCCCAGCCCTTACT	55	105	105	113	>200	1	1
91001466	pin2455	3	ATCTAGCTGGCTGTAGTAT	TAAAGAGATGAATTTATGGT	42	130	130	190	>200	1	1
91000271	pin1252	4	GTCTTGTGCTATCTGTGA	AAGCATTTATTGAGGTTTA	43	90	90	95	>200	1	3

Fig. 7

91001148	pm2256	4	GGCCAGTTTCTTAGTAT	GTCAGTTTATTCAGAGCA	42	62	62	>200	69	1	2
91001032	pm1151	4	GTCCATGCCACTGTTGTTAT	GTCTATATTCATCATCAA	43	80	80	-	-	1	1
91001215	pm0908	4	AGAAATTAATAGCATAGGT	TAGAGTCAGGTGGCTGTG	43	100	100	130	-	1	1
91001298	pm2267	4	ATCAAAATTTAATGCTTCA	CATCCCATCATACAGTGC	43	116	116	>200	180	1	1
91000993	pm0901	5	TCTCGTGAAGAGCAGCACA	TCTAAGGAGAACAGCATC	40	101	102	113	200	1	1
91000938	pm1809	5	AGCATTGCTTATCCACAG	CTAAGAGCTTGAACCTTCAT	45	87	87	>200	>200	1	1
91001085	pm0319	5	TCACCCAGATAATTACAGT	GAGACATAGCAGGTAAAT	44	120	120	-	-	1	1
91001101	pm2261	5	TTACCTTACCGTGTCTTAC	AGACAATATCCCAAAAGC	47	89	89	100	>200	1	1
91001461	pm1160	5	ATTGTTGAGTGGTTTACTA	AGAAATGATGCTTTATTC	43	101	09	>200	>200	1	1
91000053	pm2720	6	ATGTCTATAGTCTCTTCA	TGCTATCTCAATGCTCTCT	44	78	78	72	>200	2	3
91001226	pm1154	6	CATTGAGCAGCAGCAACAG	CCGTGGCCTCTCTCTAGTA	53	102	104	145	200	1	1
91001434	pm1216	8	TAGGCAAAACACGAGAGAG	AAGGAGCTGGTGTGAGTTC	48	65	65	110	>200	1	1
91001457	pm1785	6	TATATGCAATATCCAAAGTCTG	TCTAATATTCGGTCCCTTAICT	46	90, >200	90	>200	>200	1	1
91001523	pm0285	6	TTGTACGTTGTGCTCAGT	TTTAAATGTCTATGTTAAT	42	86	70	>200	100	1	1
91001525	pm0228	6	GCACCTAAGCCTCCCAAGT	TTTATATCAGTCCAGAGC	49	138	138	>200	>200	1	1
91001562	pm2619	6	TCTGCAITGACAGGAGCAC	TTTGAGATTTAATGAGTCTC	43	62	62	>200	45	1	1
91000321	pm0991	7	GACCTGAAGTGTGAATGAGT	AACCTAGCTTATGGCAITTT	45	119	119	>200	-	1	2
91001145	pm0281	7	AGCCAAAGTCGGGGTCACT	CCAGGGACAGGTGATCAT	56	159	155	115	>200	4	4
91001469	pm0219	7	AATCATTTGGCGAGACTGTA	AGACACATTTATCCAGACA	45	88	89	130	-	1	1
91001578	pm1101	7	TCAGGGAGTCTGTCAGATA	TTTGCAGGTTAATCTGTTA	44	77	76	170	-	1	1
91001207	pm0956	6	ACAGATATGCTGTGACAGTAG	TCCATTATAGGCCAGTCTTCAG	47	81	81	105	70	1	1
91001176	pm2527	9	TTGCCCTCAATGGTGTCTAC	AAACCCAAACACACATAAG	48	99	99	110	180	1	1
91001248	pm2708	8	TGTATGGAITGGATTCTC	CAAAAGCAAAACACAGATA	44	95	95	-	85	1	1
91000260	pm0995	07	TTGCCATCAAAACACATACA	CTTGTGAGTTTGGTTTCTG	43	55	55	-	-	1	1
91001055	pm0959	07	TTAAAGATCAACCCCTCATTG	CACATGCTTATGGAAACACT	44	74	74	72	73	1	1
91001157	pm0547	10	AGTATTGTGCAAGATGTA	AAGAAACACATGCCCTGTGG	45	138	139	>200	>200	2	3
91001288	pm2245	10	TGTAAATGCTATCTCTCT	GCATCTGTTCCATATCAGT	47	100	100	200	>200	1	1
91000228	pm2604	11	ATCAAAACAAACATCCAGA	ACTATATATCTGCCAACT	42	117	121	134	85	2	2
91001169	pm0800	11	GAATAGCTTGGAGATTTCAC	GGAGATCATACCTTCAGCA	46	100	100	84	95	1	1
91001315	pm0445	11	AAAGTACCTTGACAGAGTGA	TGAGCCAAATATACATGCTGACT	50	153	153	>200	160	1	2
91001352	pm2943	11	AGGGTGAAGGATTTTACG	CACATCATGGTTGAGAGCTA	47	83	85	-	-	2	2
91001469	pm0559	11	AACCTCTAGTAGGCATTG	TTATTAACCAATCCAGTA	37	47	47	125	53	1	1
91001570	pm2810	11	CTGTAAAGGTTTTGGAAATATGT	TTTCATTTTCTACAGATTATTT	42	75, 82	75	145	>200	3	3
91000279	pm0266	12	AGTGTATGGAAGACCTTGAG	GTTCAATTGAACCGGTGAGC	48	130	130	103	>200	1	2
91001163	pm2756	12	TCTGCTATTTCAGACCGAGT	ATGATTTCGTAGGATAGCA	49	88	89	>200	170	1	2
91001193	pm1193	12	CACAGATAAAGAAATCATA	ACCTTAATTAGTTTCTCAC	46	100	100	-	-	1	1
91001235	pm2790	12	CATCATGGTACAGTCAGAG	CAGTTTGTCAAAATGTAATG	44	83	82	93	87	1	1
91001274	pm1355	12	AGATGTCAGTATCTCCTCATGG	GAGAACAGCAGTAAGCAACCCAG	47	87	87	>200	>200	1	1
91001308	pm0368	12	CCAAAGTGTAGGTTACAG	TTCAATAGACCTTGGGTAC	47	95, 165	95	>200	>200	1	1
91000153	pm2645	13	CTAAGATTAATGCGATTCC	AGTTAGTGTATGCGAGAGGA	46	104	104	>200	-	1	2

Fig. 8

91001014	pm1658	13	TTGTAGCCATCATCAGATCA	AGACAGATTATGCCATCTA	44	109,200	109	>200	100	1	1
91001290	pm1731	13	GCTCTCTCTGCTGCTGGT	GCAGTTAATCATGGTATCTCC	50	122	122	>200	190	1	1
91001362	pm0118	13	ACTGAATGGAACTAGTCT	TACATACATGACATTGTGA	40	61	61	95	103	1	1
91001366	pm0364	13	TGCTAGCTTCTCCTCTTA	GAGCATTCTGTTGTCCTA	45	67	67	-	-	1	1
91001389	pm2301	13	CATGAACCTGCTCAGACAA	GCCITACTTAATGCTGACC	51	100	100	100, >200	-	1	1
91001492	pm0541	13	AAATGAATGAATAGCACT	ATTAGTTTACAGGAGAAAT	41	72	72	-	74	1	1
91001367	pm0441	14	GTTTAAGTTTGAATGGG	CATCCACTCTTACATTCT	41	77	77	>200	180	3	4
91001564	pm2307	14	CGTCTCAACTCTGAATG	AATGCTATTATCTCAAG	42	55	55	>200	>200	1	1
91001576	pm2010	14	ATCACAATTACCTTAGTTC	ACGATACCTTATGGAGAT	30	69	69	-	-	1	1
91001239	pm2220	15	TCCCATCTCAGTGAAGT	TGAGACAAAGGAACCCAGT	47	70	70	80	150	1	1
91000985	pm0985	16	TTGGAAATGGAACCCCTGCTA	ACITATGCTGCCGGAATGG	48	79	79	66	70	2	2
91001242	pm1127	16	CCCTGTGTTTACATGTTCA	TATTAATCTCCCATCAT	44	105	105	103	102	2	2
91001516	pm3543	16	ACAGTGTAAATCAAGGTG	TCTGACACCTCAAGGTGCAAT	45	70	70	>200	-	1	1
91001566	pm0913	16	TTGTGTCGGACTATGTAAT	TCACTTTAATGGGAACCAAG	41	53	53	>200	>200	1	1
91000606	pm1157	17	CTCTCCATGTCTCTACAAG	TAGAGGAGAACTGTGGTT	47	77	77	140	>200	2	3
91001015	pm2368	17	ATATCACCTTCCCATCCAT	TCAATACGCTCTCTCAAGC	50	80	80	>200	>200	1	1
91001156	pm0202	17	CAGAAATAGTGCAGCAAT	TCGTATCTGCATCTTAAGT	45	103	100	>200	>200	2	2
91001173	pm2117	17	AAATCTGTGGTTATTTCC	GTGATCTACTGTACATTC	41	118	118	145	200	1	1
91001301	pm1070	17	TAAATTTGTGGAATCTCTGGA	ACACATTTGGTTTGTCTTAAC	47	100	100	95	97	1	1
91001316	pm0511	17	TGTGACAGCAGCAGCTTCAT	TCGTACATTTAATCTCCAC	45	128	129	-	1	1	1
91001356	pm0520	17	CATCTCAGACAGCAGGAAC	ACCTAATAGTCCAGAGAAAC	40	90	90	69	>200	1	1
91001495	pm2212	17	TGACTGCAGTAAGGAGTTGT	GAACATACCAGTTATTCT	46	90	90	180	>200	1	1
91001522	pm0642	17	GTCTCAGCAGATTTCAGGT	ACTTCTCTTGAGACACA	45	68	68	160	-	1	1
91001070	pm1015	18	TGTTCTCCAGCTTTGTAG	GTTACATTCCTTGGTACAG	48	65	65	>200	>200	1	1
91001117	pm0289	19	GGATCAGACCAACAGTGGTG	GCAAGGTATAAACAGATTIA	46	50	50	-	-	1	1
91001467	pm1608	19	GAAGCCCAACCTGCACCTCA	GGAGAGTATGGGGAACGGT	54	93	93	>200	>200	2	2
91001069	pm1079	20	GCCATGCTTGAAGTGTGT	TTAAGAAGCATTAGTAGGATA	48	140	140	-	-	1	1
91001088	pm1146	20	GCCCTAGGATTCACTGCTC	ACCACCAAGGCTTTCAGG	52	66	66	180	>200	1	1
91001069	pm0112	20	TGCTGGATGACTTCACAG	TCCCTATCATGGCTGCTGT	49	59	59	59, 115	59	1	1
91001128	pm0322	20	CTGCTCGCTAGTCTGACTC	CAATGGTCTAAGAGGACAT	49	135	135	153	160	1	1
91001132	pm0647	20	TCTGATGATGATGGAAACA	ATCCTAGTCCCAACCCAGTA	48	109	109	-	-	1	1
91001156	pm1774	20	GGAGCCCATGGATTGATTG	AAATGACCCCTGGCACCTC	52	124	124	>200	>200	1	1
91001210	pm1235	20	AGCCATCTGGTTATGTTTA	GGAGCAGAAAGAACTTCAG	44	90	90	>200	>200	1	1
91001377	pm1701	21	TCCATGGTGTAGAAAGCCAG	CCACATCTCCACAGGGAGT	54	142	142	>200	74	1	1
91001395	pm2101	21	GTCAAGCTCAATGCTACACG	TTTATAGTGCACACAGAGT	45	130	130	180	>200	1	2
91001427	pm0648	21	CTTCGTGATAAAGTAGAG	ACAAITGGTTCACATAATGA	39	50	50	145	>200	1	1
91000978	pm0912	22	GGTGTAGTGAACCATTTAG	AGTTGACCCATCTCTGTC	46	124	124	>200	>200	1	1
91001444	pm0911	22	GGTCTGTCTCCCATCTGT	AGAAAGCCCAAGTAGTCC	48	65, 80	65	100	125	1	2
91001473	pm2231	22	TGAGCTGCATTACCTGTGAGAG	AAGCAGGTGAGTGGGTTTCT	50	94	94	67	135	2	4
91001479	pm2320	22	TACAGCCCTCCAGCTAAC	TTTATTCGCAICCACTACAA	48	65	65	190	>200	1	1

Fig. 9

g1000999	pm1759	X	CTGCCATAGTTACCTGGATT	TCACCCACCACATTAGCA	47	103	103	-	-	-	1	1
g1001149	pm2140	X	GGAGGGGAGATATAGATTGT	AAAAATCCAGAGACTGA	46	70	70	135	130	-	1	1
g1001161	pm0508	X	TTCTATAGTGTGACCAGTT	GGAGGATTGAGATACACAT	40	85	85	>200	77	-	1	1
g1001106	pm1791	X	TAATCCAGTGAATGTTCGGTAA	GTAAGGTTATCCTTGCATCAGA	47	02	02	>200	80	2	3	3
g1001160	pm1289	1,18	ATCTCGTGAATATACATCTG	GGGAGAGACATCACATGAC	46	70	70	68	130	-	1	1
g1001126	pm0113	1,2,12,13,Y	GATCCGATGGAGGTGAAT	AATACAGCTAAACACAA	44	69	69	170	-	-	1	1
g1001104	pm2272	1,2,3,5,9,12,14,17,X	TTGGATGACATCTCTAT	TTTATGTACAAAGCACT	43	130	130	150	132	2	2	2
g1000303	pm0314	1,2,6,X	TATCAAGCTGAATATGTCAC	TTATGTAATCCAGCCAACTA	45	93	93	110	-	-	1	3
g1000140	pm1481	1,3,4,5,8,16	TCCAAATGAAGAGGTGTTA	AGTTGACAGCCAGGTGAATG	43	96	96	100	100	1	3	3
g1001354	pm1361	2,20,21,22	GTCTGTCAAGCCAAATGCA	TTTTTATGTGCTCCAAGT	43	110	110	170	150	1	1	1
g1000326	pm2795	2,4,5,10,12,15,17,20,22,Y	GACCTGTGACATCTGGACT	TTATATGTTGTACACATCG	43	61	61	-	-	2	6	6
g1001077	pm0912	2,5,14,C	GCTTGTATTCACCACTC	ATCCCTTTGCTCCAGTTA	46	82	82	>200	82	1	1	1
g1001192	pm1653	2,9,12	TCTGAGCACATCCAAAGACG	CAGTCAAACCCACCGGTAT	49	95	95	93	160	1	1	1
g1000213	pm1776	2,9,13,17,X	TGCAATAAAGGGAAAGACCA	CCGTGTAGGTGATGAATG	49	78	80	>200	>200	1	2	2
g1000919	pm0885	20,X	GTCATTGTATGCCATTCC	ACATTTTATTTTTCACGG	37	45	45	-	-	1	2	2
g1001109	pm0457	3,10,15	CATGTACTCAGAGGCCTTC	GCACCTACAGGAGATGTTAC	50	133	133	>200	150	2	2	2
g1000071	pm2651	3,4,M	CAGGGACTGGAGCAGGAAG	GATTTACCCATAGGAAGC	50	101	101	101	88	3	3	3
g1001126	pm2632	3,6	TTAGGAAATATGGTTAGACAG	ATAGTATGGGTGTGACACAGTA	43	80	80	>200	120	1	1	1
g1001139	pm1133	3,8	TGGATTGCTTACCTTGTT	ACACCTCAGGAGATGTTAC	47	93	93	95	>200	1	1	1
g1000377	pm2750	3,9,10,15	GCACACAGCCAAATCAGA	CTCTTACACCAACAGCAG	50	96	96	>200	175	2	10	10
g1000605	pm0626	4,6	GGATTCTATTGCTGTCAT	GTTATTTGACGGCATTTAC	44	105	100	>200	>200	2	4	4
g1001212	pm1234	6,20	GCATTAAAGGAAACAATA	CTGTCCAIGTGGCATAACE	44	110	110	105	107	1	1	1
g1001312	pm0606	7,18	AGATGCTAATAGGGGATA	TTTTAGACATACAGAGGAGT	43	81	81	102	-	1	1	1
g1001441	pm1253	9,11	CCAGACTACAGGCTGATGGC	CCCTACCCCAACCACTCT	55	75,130	75	>200	>200	1	1	1
g1001357	pm0115	9,M	ACCAATGTCATGCTCTAATAA	CCCAATATAGTGAAGGTAGTTTC	48	135,155	127	125	>200	1	1	1
g1001261	pm0428	10,15,22	AGAAATGTGTTTACTGGATT	TTATCTGACTTGGAGGAAT	42	107	107	-	-	1	1	1
g1001154	pm2120	10,15,22	ACTACCCTGADATATTAGTT	TTCATTTATTTGATTGTA	46	100	100	170	-	1	1	1
g1000750	pm2303	11,M	ATACCAGTCCGCTGTCAGG	GAGGAGGCTCTACTGGCTTT	50	72	74	72	>200	3	20	20
g1003114	pm2613	12,19	GCACCAAGAGCCAGTCCAG	TTGGGAATGAGAAATAACT	46	83	83	81	-	1	7	7
g1003103	pm2773	12,M	GATCTCAGTCTGGCTTTATT	TACATCAAAAGATCCAAACAGT	44	80	80	70	68	1	1	1
g1001487	pm2725	13,16	ATCTGTGTGCTGCTTCC	GTCTCTCTCTGATGGCTGA	46	62	60	135	180	1	1	1
g1003276	pm2780	14,16	AACCTGTTTACCCGATCTT	AGGTATTGTGTCACCAAGAA	48	87	87	>200	>200	1	1	1
g1001435	pm1683	17,20,C	TGTTGGTTCACCATTTGAGAC	AGAACACATCAAAAGATGC	46	90	90	>200	90	1	1	1
g1000356	pm1748	17,22,Y	GAATGTCATCCAGAGCTAG	CTAGTTATCTCTGGCTCTG	44	81	81	>200	200	1	1	1
g1000964	pm0964	17,C	TTATCCAGCAAGCAGAAC	TCTCTCTCTCCTCTCTC	49	120	120	>200	170	4	11	11
g1002117	pm2217	17,C	ACTTAAAGTAGCTTTGTACG	TGCTCTCTGCTGATATA	43	95	95	>200	95	1	1	1
g1003140	pm1213	18,C	CCCAGTTAAAGATTATTGT	AGTGACGATGGAAGGATGTA	44	92	92	-	92	1	1	1
g1001217	pm1116	19,20	TGCAGATGATTTCACGAG	CGTAGGTCATCTTTTCAGC	46	75	72	160	65	1	1	1
g1001009	pm2824	19,22	ATCCCTGCTCTATTCACAG	GCTCGTTAACTCCTCCTCAG	46	110	110	130	170	2	2	2
g1001172	pm0887	19,22	GCTGTCATCTGTGTGACTT	AACCTCTGGGAACAATCAI	48	91	89	160	86	1	1	1

Fig. 10

9-031057	pml2049	C	AGGACACAAACACCAGCTAT	TTTCTGATATGACATGAC	45	75	75	101	75	1	1
9-000173	pml1753	M	ATCTCTTGAGCCATCCTG	GTTAAAGTCTGATGCCATT	42	64,100	64	64	>200	1	1
9-031096	pml2236	N	GTAGAGCTGCATTGACTACC	ACAGACAAGGAATATCATTA	42	100,98	110	110	112	1	1
9-031166	pml0506	N	GTCCACAGTCCAGCCTAAC	GCCACATATTAGAAATCCATC	46	74	74	74	>200	1	1
9-001151	pml2354	M	TGCTTTGTGGAGTCTGGCT	TTTAAAGTCAATAATACATGTT	44	110	110	110	106	1	1
9-030229	pml2492	M1C	GCTAGAAAGAGGCACTCA	CTAACTCGATAGCCAGGTC	46	75	75	75	75	1	1
9-030253	pml2786	M1C	CACAAACAGCAACTTCAG	ATGGTTATTATACAGATTG	41	83	83	82	83	2	3
9-000285	pml1704	M1C	TCCACCCAGAGAACACACT	AAITCATGGGAATAGGTTG	40	75,130	75	75	75	1	23
9-000543	pml2318	M1C	TGGAGAGGAGCAAAATCACC	GAACAGGTTAGTCCATTCG	40	50	50	50	50	1	1
9-000675	pml1609	M1C	CATGAGGCTAGCGAACAGG	AGGAGTCCGTGGGTCTTGAG	51	81	84	84	84	4	18
9-000732	pml1442	M1C	AAAGCATCTGAGAGGAACA	GGAGGACTGGCTGGGTCTTA	49	110, >200	110	110	110	1	9
9-000995	pml1452	M1C	GCAGCAGATACCTITACACC	TGGTTCAATTGAGTTCCTTC	51	102	105	102	102	3	13
9-001016	pml268	M1C	GAAGCTCTGTGAGGAAGT	CAGACCCCATCTTTATACC	47	79	79	79	79	3	4
9-001053	pml2783	M1C	ACGATATTATAGTCAATG	TCAAACTTTAATATATGCT	40	93	93	91	92	1	1
9-001127	pml1144	M1C	AGATGAGTGTGGTTCAGAGA	CCATTCCTTCATTCAGTT	52	135	140	135	135	1	1
9-001127	pml2290	M1C	ACTGTGATGAGAGGTTACA	CCACACAGTGAACACCTCT	47	55	55	55	55	1	1
9-001127	pml1626	M1C	GAGAGCCCTGCACTCCTTA	CTTCCCTTTGGTCTTCTGT	49	100	100	100	100	1	1
9-001216	pml1209	M1C	TAGTCAGAGATCAGTAAGT	ACATGTAITTTGATAGTCTT	42	110	110	110	110	1	2
9-001253	pml1240	M1C	AACTGGTTCATCAAGACTG	AGTGAATAACCTCTCCACTCC	48	120	120	120	120	1	1
9-001281	pml1131	M1C	ACTTAAAGCCCAAGCAT	ACACAGCAGTCAATAGAA	47	97	97	97	97	1	1
9-001375	pml0952	M1C	AAGAGGAGTTTCCCTCTCA	ATCATCTTTTATTTGACAT	51	89	89	89	150	1	1
9-001356	pml2216	M1C	ATCGCATACCTATATCT	GAGACCAAGGCACTCTTA	45	108	108	108	108	1	1
9-001411	pml0958	M1C	ATGGTTATCAGGGTTTC	GGACATTTCTAGCCACAGC	47	80	77	80	80	1	1
9-001420	pml2826	M1C	ACATGAATGGGATGAGGT	GGACATTTCTAGCCACAGC	51	75,55	75	75	75	1	2
9-001482	pml1210	M1C	TTGTTGACATCTTTTAGAA	CAGTGCCTCTGTACTGAGACA	46	85	85	85	85	1	2
9-001450	pml0109	M1C	GCCACACAGAGACATCCT	TCTTAGAGTGTCTGGTGG	51	98	98	98	98	1	1
9-001488	pml2042	No product	CAACAGTTAGCGTGAAGT	GAATAATCTCTGTCATCTA	45	87	87	-	-	1	1
9-000450	pml0304	No product	CTTTGGGATATTTCTTCAT	CCCTCGGTACTTTCTATG	43	60	60	62	-	1	2
9-000683	pml0808	No product	AGCCAGCCTCTTGTATGTG	CTGGATTGATTTTCATAG	44	87	87	-	-	1	1
9-001254	pml1673	No product	TGTGTATGAAATATCTGA	TTATGAATGAAGACACACT	43	98	98	163	>200	1	1
9-001365	pml2008	No product	CAGTAGTGTGCTTGAATG	TTATGTGAATGTGTTGT	41	63	63	-	150	3	3
9-001373	pml0761	No product	TACAGCCCTTCTAAAGTC	TTTGAGCATCAAGGAATCT	46	82	82	-	>200	1	1
9-001556	pml0849	No product	TACATCTTCAGACTCATCG	TTTCAAACTTTATCTT	40	86	86	>200	100	1	1
9-001574	pml1284	No product	ATCAGAGCTCAGTCTGTAG	ATTTCCTCTTGCATGGTC	44	57	57	67	67	2	2
9-001622	pml1606	No product	GATCTGAGCCTTAACGGA	TTTGCAGTTCAGCTTATTC	45	54	54	-	-	1	1
9-001640	pml0552	No product	GATCTGTGCTTCTTTCACA	TTTATACAGACACCATAC	36	45	45	-	-	1	1

Fig. 11

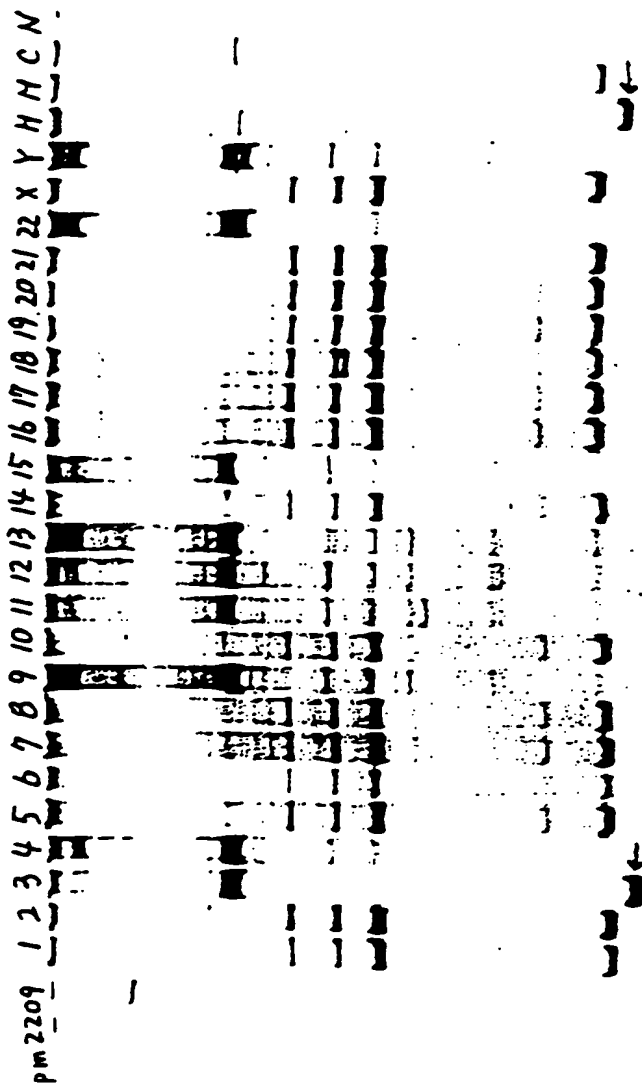


Fig. 12

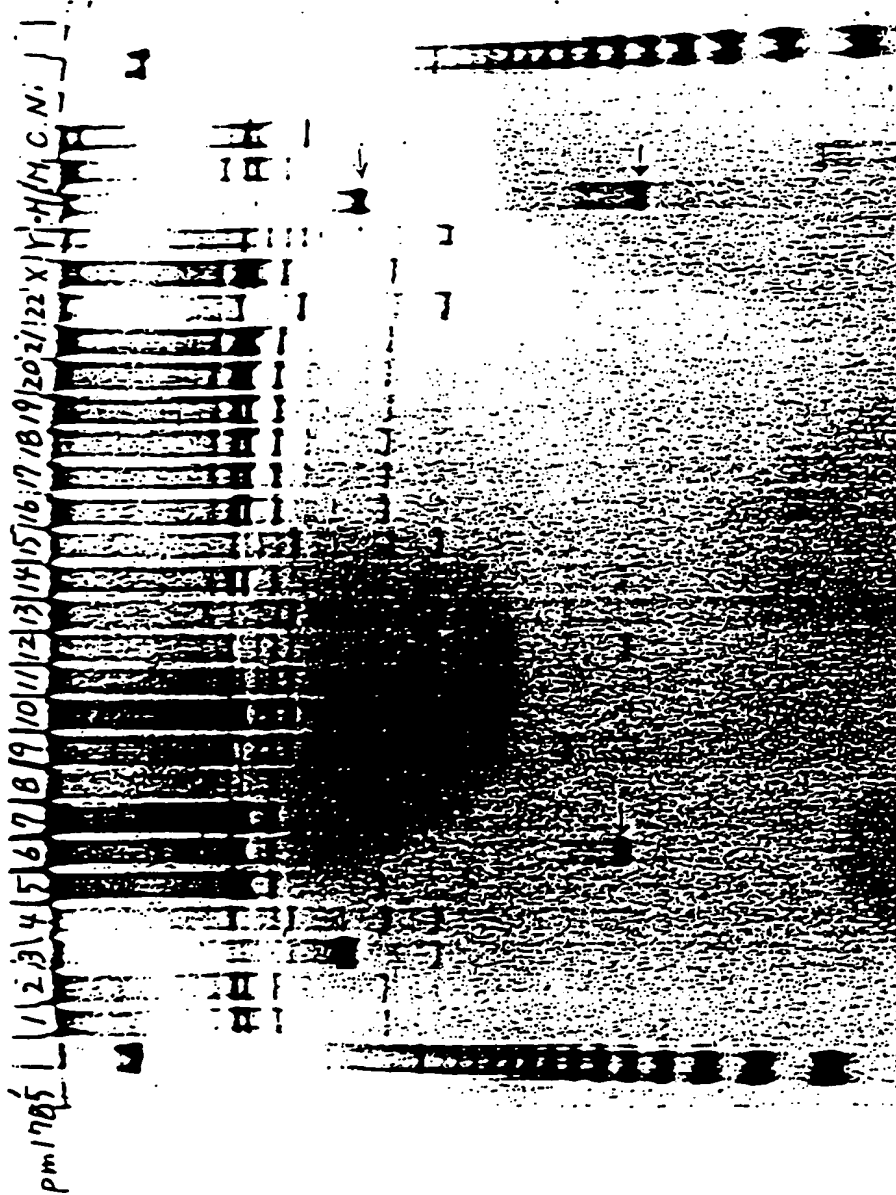


Fig. 13

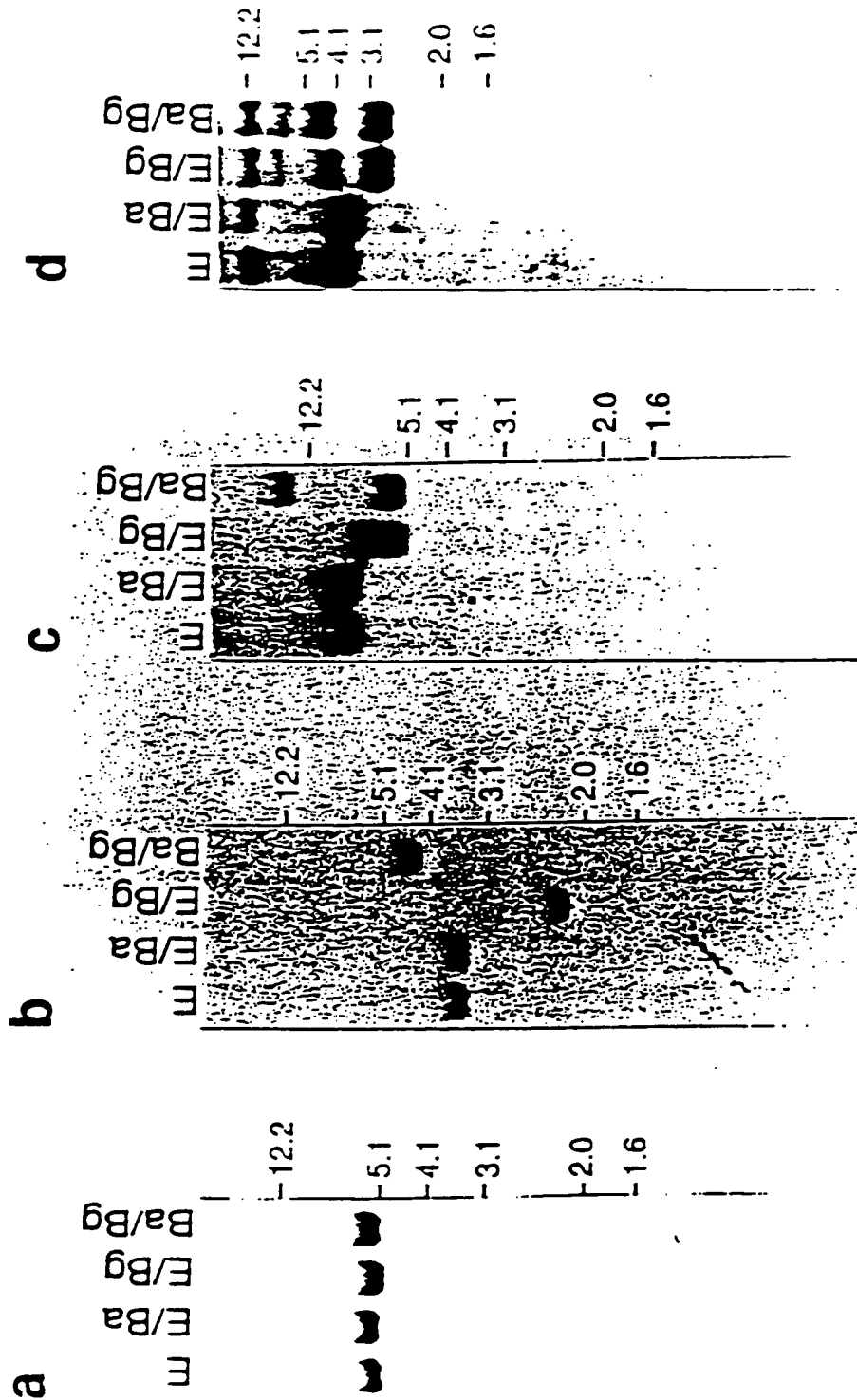


Fig. 14

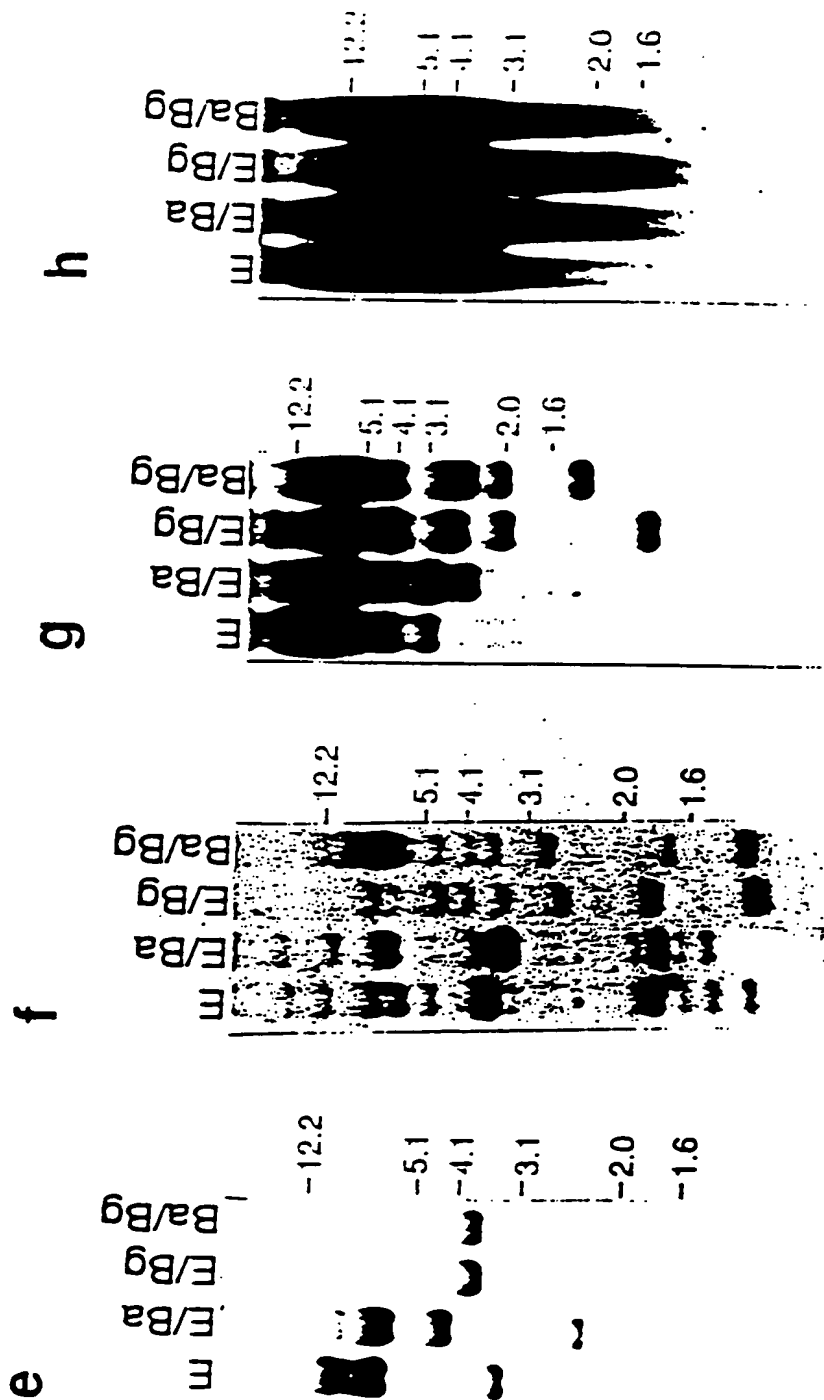


Fig. 13

Hybrid cells used for Southern hybridization

Hybrid cell	Human chromosome No.	Parent cell	Intact chromosome (%)	Translocated chromosome (%)
A9(neo-1)-4	1	A9	100 (0)	0
A9(neo-2)-1	2	A9	93 (8)	0
GM10253	3	CHO	100 (0)	0
GM10115	4	CHO	100 (0)	0
A9(neo-5)-4	5	A9	40 (0)	90
A9(neo-6)-3	6	A9	100 (60)	0
A9(neo-7)-2	7	A9	100 (89)	0
A9(neo-8)-1	8	A9	91 (82)	0
GM10611	9	CHO	79 (5)	11
A9(neo-10)-3	10	A9	94 (6)	75
A9(neo-11)-1	11	A9	24 (0)	76
GM10927A	11	CHO	96 (21)	4
A9(neo-12)-4	12	A9	0 (0)	100
GM10868	12	CHO	82 (6)	0
GM10898	13	CHO	82 (0)	10
GM10479	14	3T6	76 (29)	0
A9(neo-15)-2	15	A9	9 (0)	78
GM11418	15	CHO	62 (0)	100
GM10567	16	A9	69 (0)	0
GM10498	17	LTMK	80 (10)	0
A9(neo-18)-5	18	A9	100 (66)	0
A9(neo-19)-1	19	A9	92 (23)	8
A9(neo-20)-3	20	A9	81 (5)	17
GM08854	21	A9	81 (24)	0
GM10027	22	CHO	93 (0)	100
GM10324	X	A9	81 (10)	0
GM06317	Y	CHW1103	91 (0)	9

Fig. 16

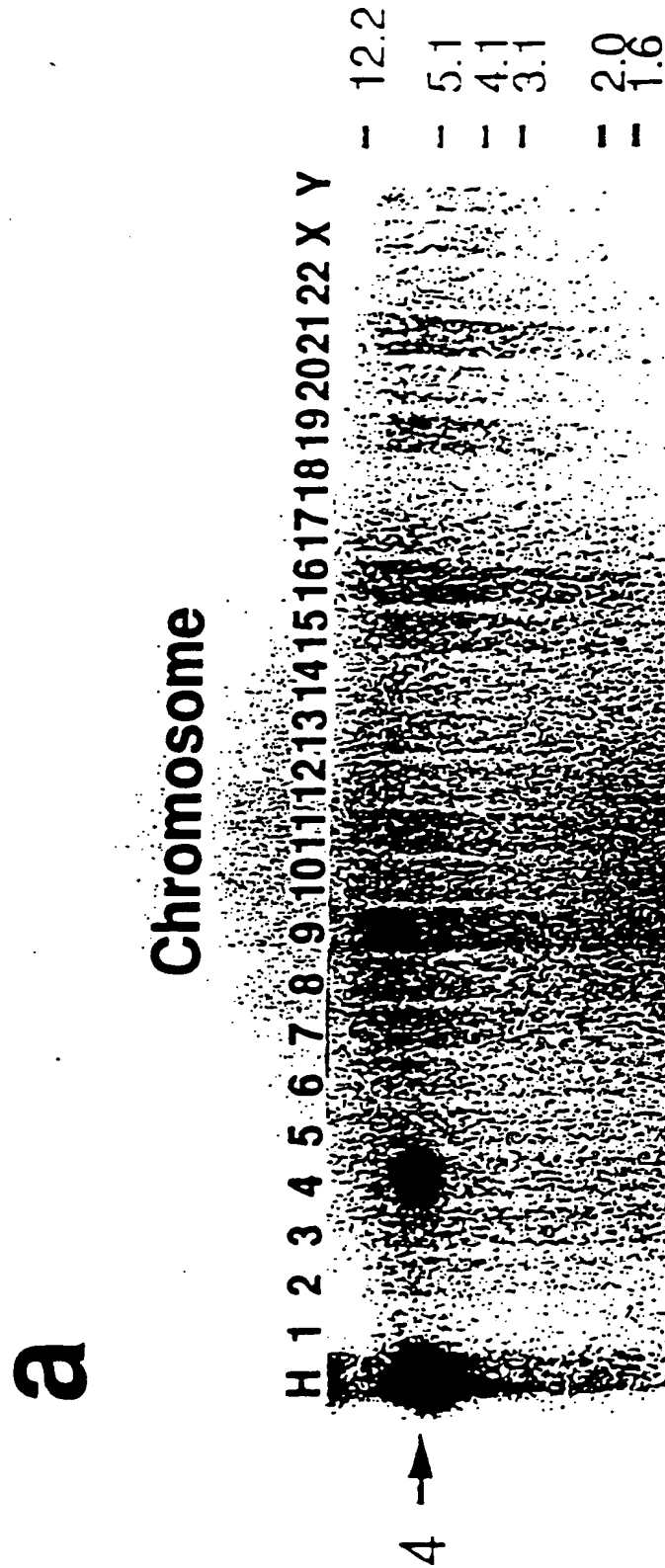


Fig. 17

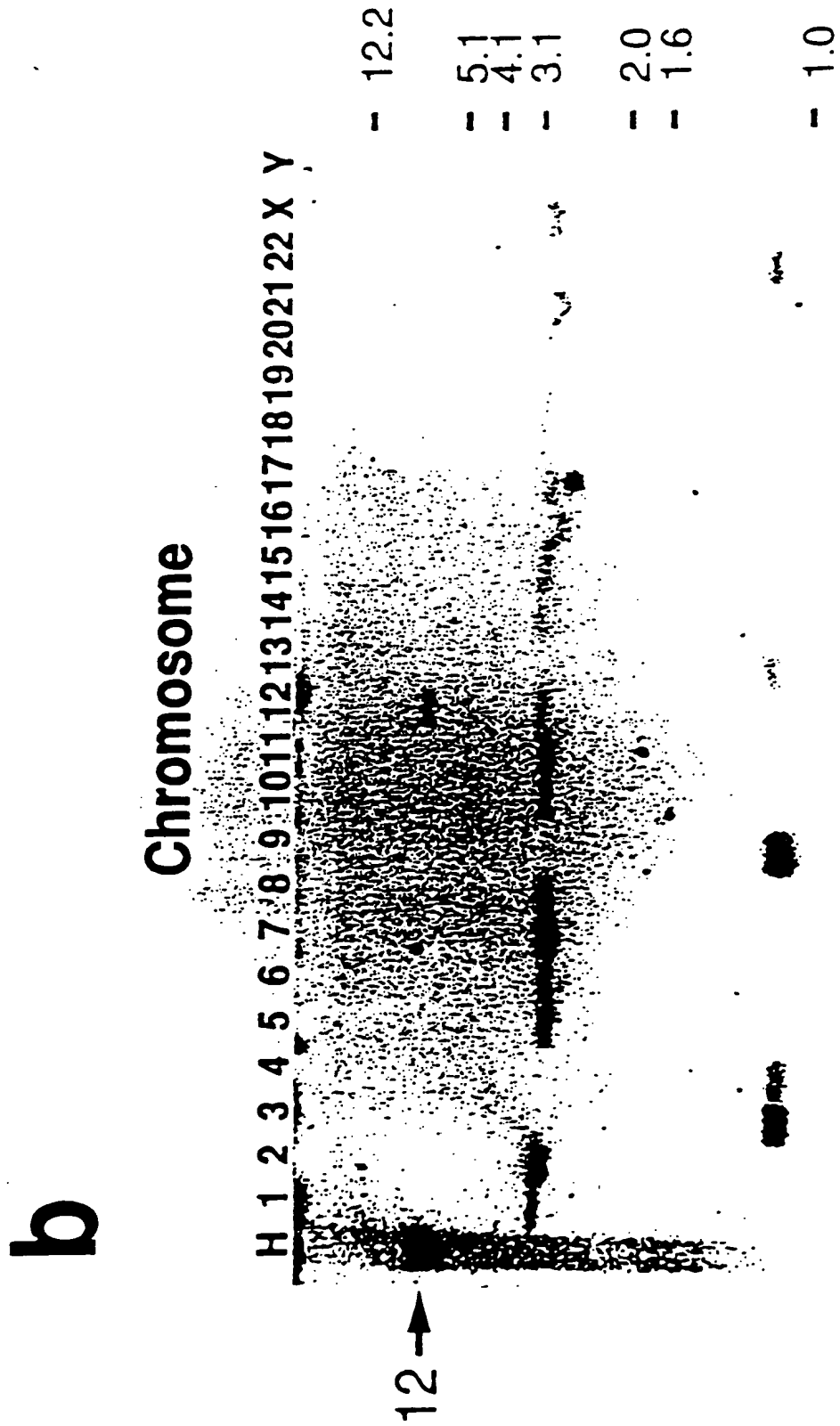


Fig. 18

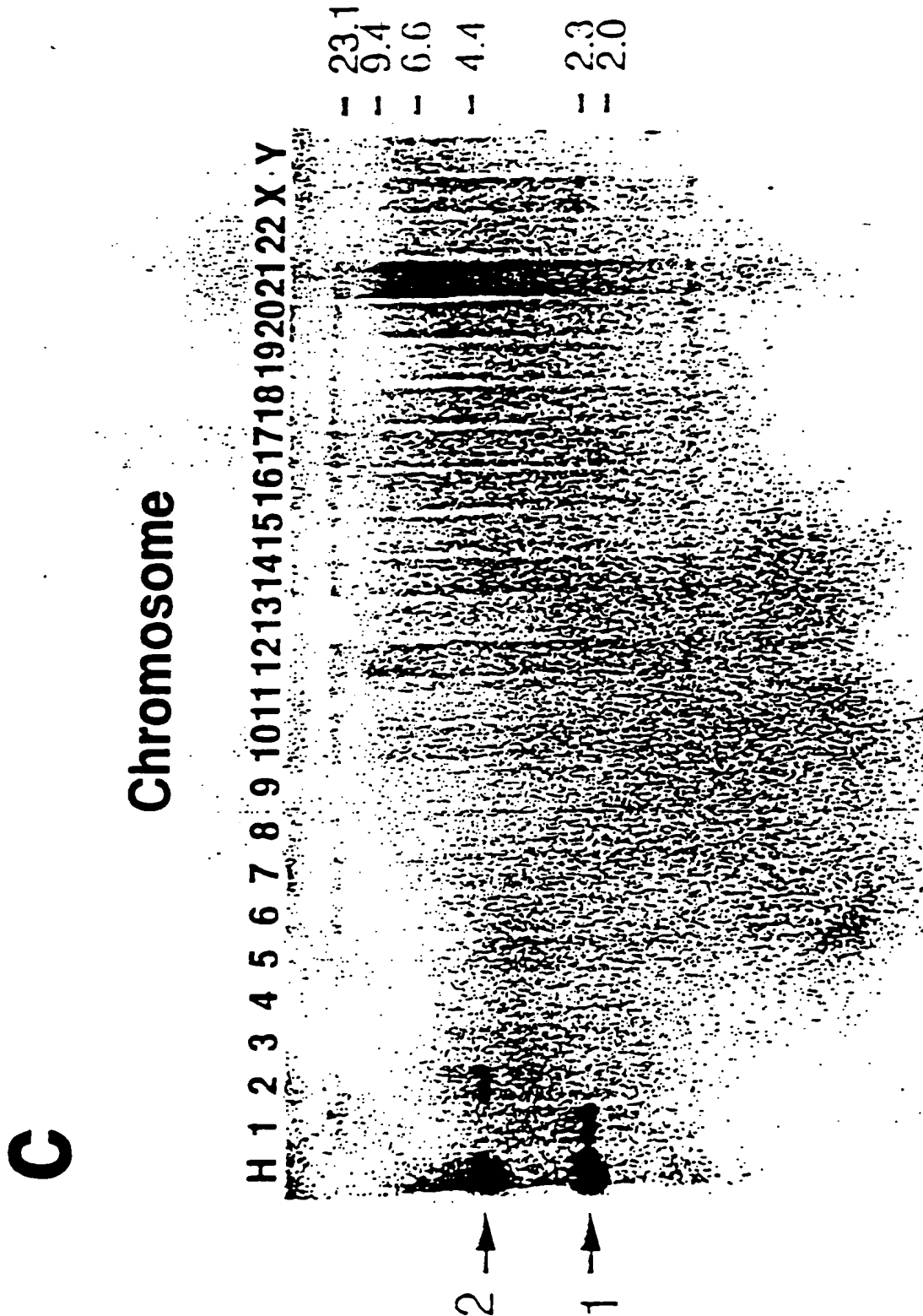


Fig. 19

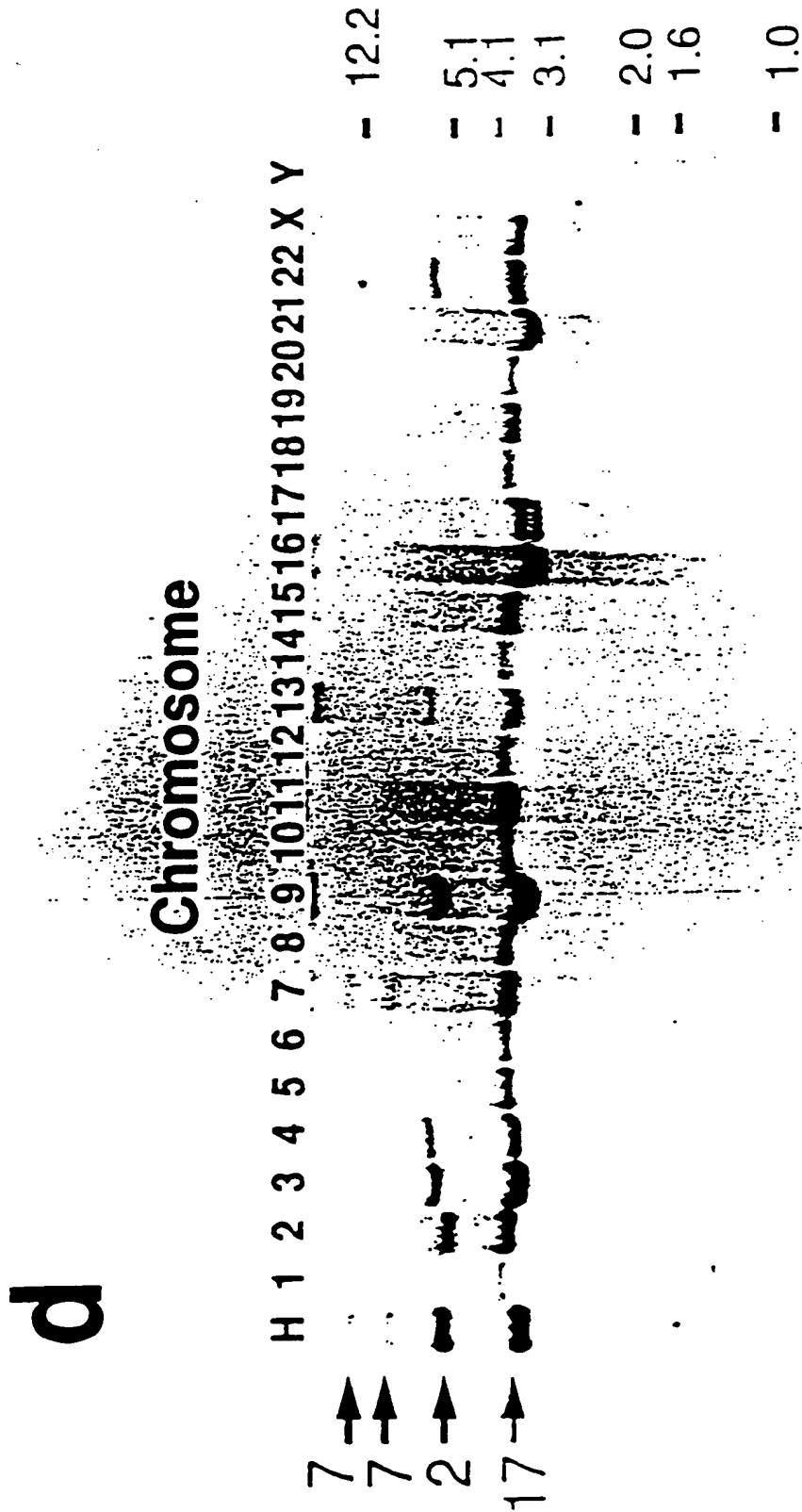


Fig. 20

e

Chromosome

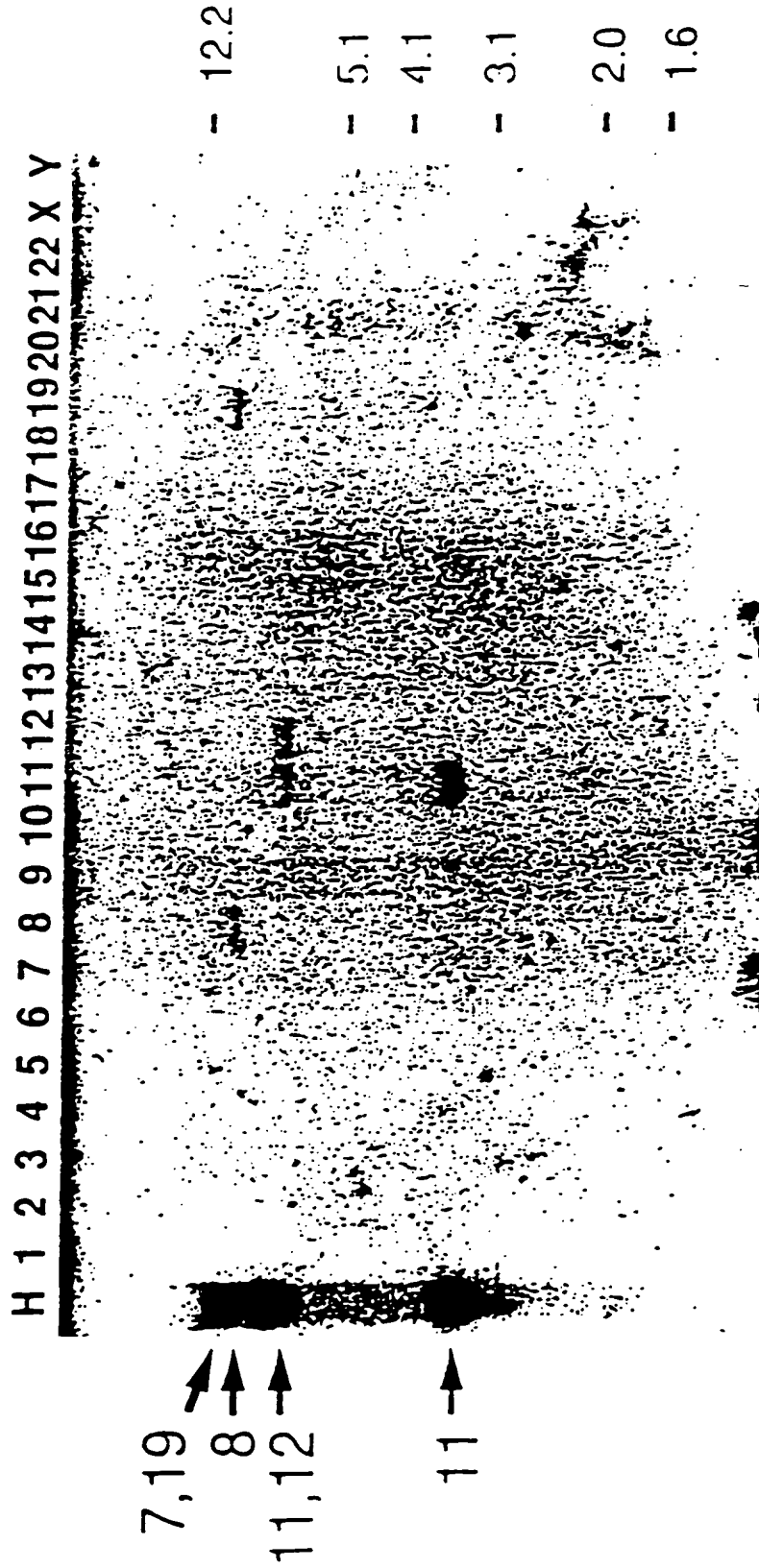


Fig. 21

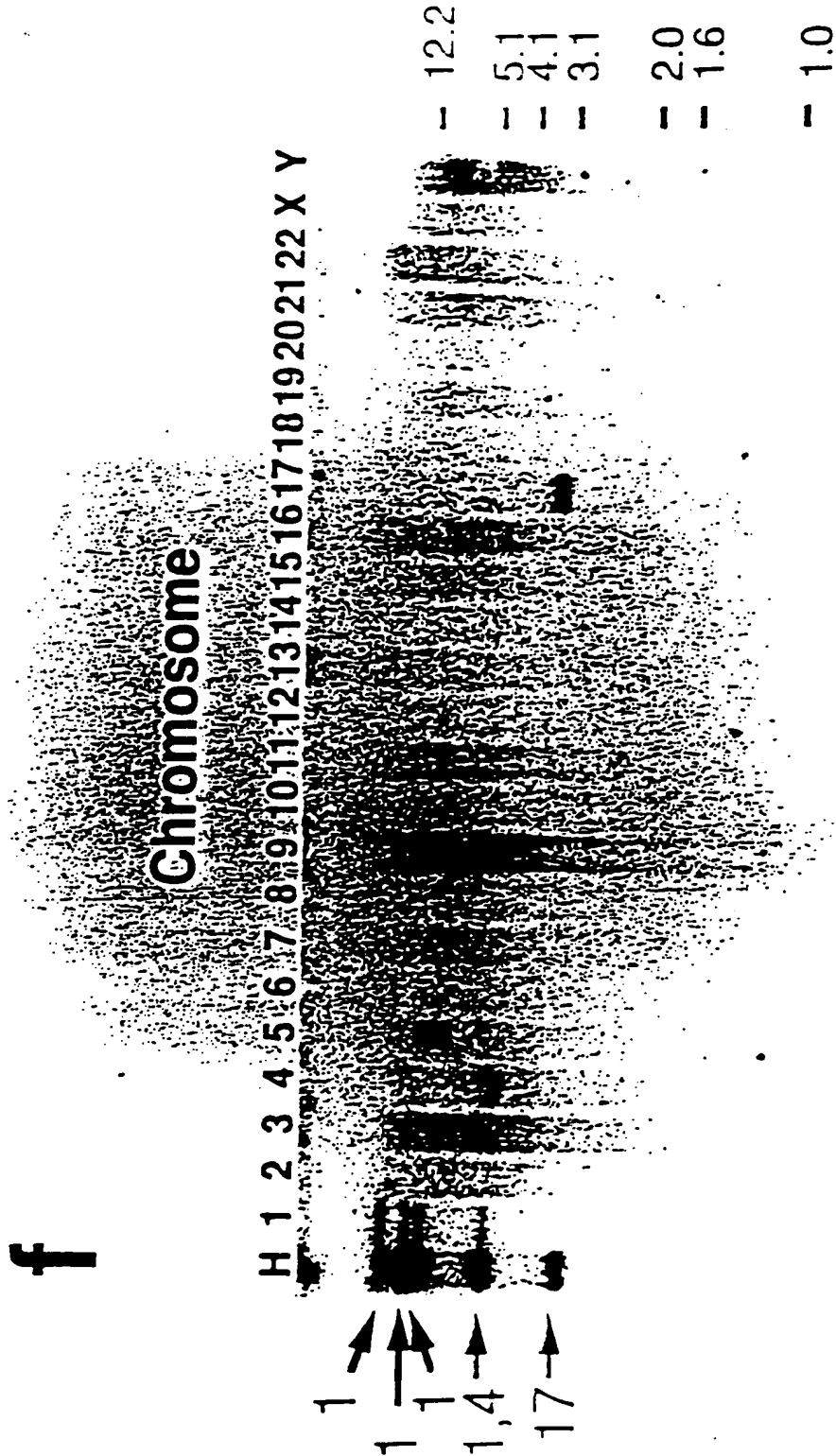


Fig. 22

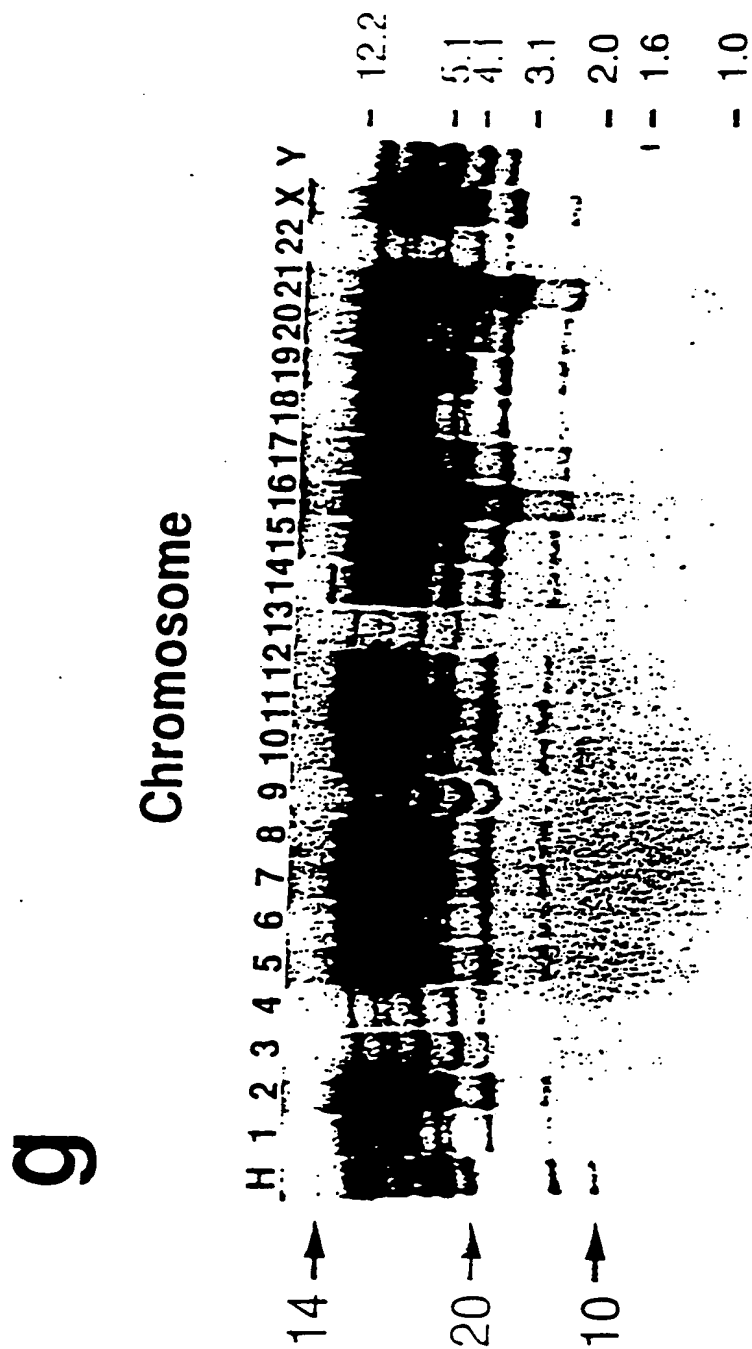


Fig. 23

Chromosomal mapping of each GS by Southern blot technique

Numbers of bands detected with human whole chromosomes					Chromosomes assigned		Background		
Clone	Sequence length	2	2/3	2/3	3/4	3/4	Mouse	Chinese hamster	
Single band group:									
c12e11	GS000075	432	1	1	1	1	9	0	0
c12e06	GS000062	540	1	1	1	1	6.15	0	0
c12g01	GS000290	212	1	1	1	1	2	1	1
c13e05	GS000117	359	1	1	1	1	11-	0	0
c13e07	GS000120	355	1	1	1	1	2	0	0
c13f10	GS000206	257	1	1	1	1	14	0	0
c13h01	GS000279	133	1	1	1	1	12-	0	0
c13h02	GS000322	167	1	1	1	1	6	0	0
d0g02	GS000095	397	1	1	1	1	3	0	0
d0h07	GS000154	313	1	1	1	1	11	1	1
d1b10	GS000348	153	1	1	1	1	20	0	0
hm01e12	GS000223	246	1	1	1	1	27	0	0
hm01e09	GS000423	157	0	1	1	1	1	0	0
hm01e12	junk	394	1	1	1	1	17	0	0
hm01f05	GS000066	454	1	1	1	1	19.22	0	0
hm01f10	GS000299	173	0	1	1	1	10	0	0
hm01g09	GS000053	477	1	1	1	1	6	0	0
hm01h07	GS000115	363	1	1	1	1	12	0	0
hm02a02	GS000130	344	1	1	1	1	4	0	0
hm02a04	GS000329	164	1	1	0	0	10	0	0
hm02e01	GS000293	271	1	1	1	1	15	0	0
hm02e01	GS000013	590	1	1	1	1	20	0	0
hm02e02	GS000342	156	0	1	1	1	14	0	0
hm02e05	GS000401	223	1	1	0	0	n.d.	0	0
hm02g02	GS000191	273	1	1	1	1	17	0	0
hm05e05	GS000251	219	1	1	1	1	6	2	0
hm05e10	junk	392	1	1	1	1	1	1	1
hm05e10	GS000009	606	1	1	1	1	1	0	0
km001	junk	169	1	1	1	0	n.d.	0	0
s105	GS000001	703	1	1	1	1	5	0	0
s110	GS000037	471	1	1	1	1	8	0	0
s11d11	GS000307	#175	0	0	0	1	7	0	0
s11h01	GS000269	204	1	1	1	1	3	0	0
s147	GS000060	461	1	1	1	0	2	0	0
s14e06	junk	639	1	1	1	1	1	0	0
s14g02	GS000152	322	1	1	1	1	4	0	0
s14h12	GS000271	193	1	1	1	1	4	1	1
s150	GS000143	330	1	1	1	1	17	0	0
s156	GS000002	306	1	1	1	1	2	1	1
s15b11	GS000250	221	1	1	1	1	14	0	0
s179	GS000275	196	1	1	1	1	n.d.	0	0
s246	GS000224	241	1	1	1	1	9	0	0
s247	GS000347	153	1	1	1	1	1	0	0
s270	junk	135	1	1	1	1	19	0	0

Fig. 24

Numbers of bands detected with human whole chromosomes			Chromosomes assigned				Background		
Clone	Sequence length	2	2/3 ₁	2/3 ₂	3 ₁ /3 ₂		Mouse	Chinese hamster	
s306	GS000256	205	1	1	0	1	X	0	0
s309	GS000171	305	1	1	0	1	1	0	0
s342	GS000323	165	1	1	1	1	4	3	2
s331	GS000255	207	1	1	0	1	6,15	1	1
s334	GS000165	312	1	1	1	1	1	0	0
s337	GS000276	195	1	1	1	1	17	0	0
s339	GS000235	130	1	1	1	1	a.d.	0	1
s443	GS000330	251	1	1	1	1	a.d.	0	0
s470	junk	251	1	1	1	1	17	0	0
s474	GS000192	273	1	1	1	1	5	0	0
s503	junk	312	1	1	1	1	12	0	0
s507	junk	600	1	1	1	1	1	2	1
s517	GS000334	161	1	1	1	1	14	1	1
s632	junk	587	1	1	1	1	2	0	0
s633	GS000166	311	1	1	1	1	22	2	1
s650	GS000041	644	1	1	1	1	12	1	1
tw1-04	GS000025	537	1	1	1	1	3,7	0	0
tw1-19	GS000213	255	1	1	1	1	17	0	0
tw1-32	junk	250	1	1	1	1	5	0	0
tw1-37	GS000237	235	1	1	1	1	22	0	0
tw1-42	junk	391	1	1	1	1	8	1	1
tw1-43	GS000095	173	1	1	1	1	14	0	0
tw1-96	GS000133	339	1	1	1	1	11	0	0
Two band group:									
c12f12	GS000195	277	1	2	2	2	1,	1	1
c13d02	GS000042	503	2	2	1	1	2,	0	0
hm01a06	GS000129	344	2	2	2	2	11,13	3	5
hm01a07	GS000207	269	2	2	2	2	7,	0	0
hm01d05	GS000232	243	2	2	2	1	2,	0	0
hm01e01	GS000181	292	2	2	2	2	1,2	0	0
hm02a08	GS000435	302	2	2	2	2	3,	1	1
hm02c04	GS000221	253	2	2	2	2	3,	0	0
hm02c05	GS000146	332	2	2	2	2	17,19,22	0	0
hm03f07	GS000043	503	1	1	2	1	3,	0	0
s11d06	GS000268	205	2	2	2	2	11,12	0	0
s11g12	GS000337	255	2	2	2	2	6,	0	0
s124	GS000083	404	2	2	2	2	9,	1	1
s144	GS000132	342	1	2	2	2	1,7	0	0
s14f03	GS000239	243	1	2	2	2	2,	3	2
s15e02	junk	439	2	2	1	2	6,	0	0
s16b09	junk	420	1	1	1	2	10,14	0	0
s17c09	GS000248	223	2	2	2	2	14,	0	0
s231	junk	284	2	2	2	2	11,	0	0
s254	GS000124	353	2	2	2	2	1,	3	1
s255	GS000235	239	2	2	2	2	11,	0	0
s272	junk	195	2	2	2	2	10,16	1	1

Fig. 25

Numbers of bands detected with human whole chromosomes			Chromosomes assigned				Background	
Clone	Sequence length	E	E/B ₁	E/B ₂	3 ₁ /B ₁		Mouse	Chinese hamster
s311	CS000092	333	1	1	2	2	16.	1
s313	junk	132	2	2	1	0	20.	0
s317	CS000100	339	0	0	1	2	14,14	1
s336	CS000134	337	2	2	2	2	12,14	0
s333	CS000139	233	2	2	2	1	22,X	0
s339	CS000233	137	2	1	1	2	17.	0
s394	CS000063	449	2	1	2	2	13,14	0
s396	junk	277	2	2	2	2	17.	0
s455	junk	452	1	2	2	1	4.	0
s456	CS000236	132	2	2	2	2	8,10	1
s465	CS000201	274	1	1	2	2	6,15	0
s635	junk	250	1	1	1	2	9,13	0
s639	CS000257	205	1	2	2	2	2X	0
s656	CS000025	#590	2	2	0	2	6,11	0
twl-33	junk	352	2	2	2	2	1.	0
twl-39	CS000153	#321	2	2	2	2	17.	0
twl-70	CS000061	441	1	1	2	1	11.	0
twl-80	junk	453	2	2	1	2	9,17	2
twl-87	CS000158	316	2	2	2	2	7.	0
Three band group								
d0h06	CS000030	417	3	3	3	1	1.	0
hm05b07	junk	336	2	3	3	3	5.	0
hm05g02	CS000299	267	2	2	2	1	3,17,19	1
s129	CS000107	373	3	3	3	3	n.d.	1
s173	CS000357	146	1	2	2	3	2.	0
s17a10	CS000294	131	3	3	3	3	2,13,22	1
s308	CS000412	638	2	2	2	3	XX	1
s401	CS000224	249	2	3	3	3	6,6.	0
s654	CS000045	491	3	3	3	3	1,22.	0
twl-82	CS000203	267	3	3	3	3	13.	4
Four band group								
cl2g07	CS000154	320	4	4	2	3	5, 14.	0
cl3a08	CS000055	508	3	3	4	4	2,7,7,17	1
cl3c04	CS000106	#376	4	3	3	3	n.d.	0
cl3c09	CS000302	195	4	2	4	4	2,17.	7
s136	CS000160	315	4	4	4	4	4X.	2
s163	CS000004	#618	4	4	4	2	4,4,8,20	3
s479	CS000130	293	4	4	2	2	7,8,11,11,12,19	0
Group with 5 or more bands								
cl2f08	CS000253	217	5	5	5	2	2,7,9,14.	2
hc01	junk	374	12	12	15	13	1,2,6.	22
hd10	junk	361	4	4	4	8	n.d.	12
he10	junk	173	6	2	3	3	6,3,9,19,21.	3
hm01c05	CS000305	176	9	7	5	5	X	9
hm01f04	CS000246	315	8	10	5	5	n.d.	12
hm01g02	junk	411	9	6	6	4	10,14,20.	14

Fig. 26

Numbers of bands detected with human whole chromosomes					Chromosomes assigned		Background		
Clone	Sequence length	Σ	Σ/3 ₁	Σ/3 ₂	Σ/3 ₃		Mouse	Chinese hamster	
hm02f09	GS000273	442	3	7	7	5	3,3,6,11,13,14,15,16	0	0
hm05a02	GS000096	373	3	6	4	6	2,3,17	3	3
hm05a04	GS000236	#239	6	6	6	7	n.d.	8	5
km501	junk	350	3	5	5	5	13	14	7
s11f06	GS000316	170	6	6	6	4	1,2,2,3,4,6,13,15	0	3
s14f01	GS000407	262	12	11	10	9	1,5,9,13	6	3
s173	GS000094	397	5	4	6	8	1,1,1,1,4,17	0	0
s255	GS000323	167	10	12	11	14	13	9	5
s341	junk	494	9	9	8	6	n.d.	15	3
s406	GS000113	364	6	7	5	4	2,7,8,13,20,20	4	1
tw1-46	junk	593	9	10	10	10	1,1,2,2,5,11,X	3	5
tw1-43	junk	203	8	10	10	12	3,4	17	11
Bands no detected:									
cl3g02	GS000340	157	0	0	0	0	-	-	-
hm01e10	junk	232	0	0	0	0	-	-	-
hm02d11	GS000274	196	0	0	0	0	-	-	-
s323	GS000273	194	0	0	0	0	-	-	-
s359	GS000199	279	0	0	0	0	-	-	-
s511	junk	233	0	0	0	0	-	-	-
s645	GS000012	#734	0	0	0	0	-	-	-
s647	GS000105	360	0	0	0	0	-	-	-
s651	junk	540	0	0	0	0	-	-	-

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int. Cl⁶ C12N15/11, C12Q1/68//G01N33/566

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

BIOSIS PREVIEWS, CAS ONLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids. Res., Vol. 15, 1987, Ou, J. H. "Cloning and characterization of a human ribosomal protein gene with enhanced expression in fetal and neoplastic cells" p. 8919-8934	1-6 (164)
X	Differentiation, Vol. 33, 1986, Oshima, R. G. et al. "Comparison of mouse and human keratin 18:A component of intermediate filaments expressed prior to implantation" p. 61-68	1-6 (226)
X	J. Biol. Chem., Vol. 265, 1990, Wilkin, D. J. et al. "Isolation and sequence of the human farnesyl pyrophosphate synthetase cDNA: coordinate regulation of the mRNAs for farnesyl pyrophosphate synthetase, 3-hydroxy-3-methylglutaryl coenzyme A reductase, and 3-hydroxy-3-methylglutaryl coenzyme A synthetase" p. 4607-4614	1-6 (255)

☒ Further documents are listed in the continuation of Box C.
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Date of the actual completion of the international search

February 6, 1995 (06. 02. 95)

Date of mailing of the international search report

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Batra, S. K. et al. "Molecular cloning and sequence analysis of the human ribosomal protein S16" p. 6830-6833	1-6 (275)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Ben-Ishai, R. et al. "A human cellular-sequence implicated in trk oncogene activation is DNA damage inducible" p. 6039-6043	1-6 (313)
X	J. Biol. Chem., Vol. 263, 1988, Fischer, R. et al. "Multiple divergent mRNAs code for a single human calmodulin" p. 17055-17062	1-6 (386)
X	J. Cell Biol., Vol. 108, 1989, Barnett, T. R. et al. "Carcinoembryonic antigens: Alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic antigen family" p. 267-276	1-6 (446)
X	J. Biol. Chem., Vol. 265, 1990, Natsumeda, Y. et al. "Two distinct cDNAs for human IMP dehydrogenase" p. 5292-5295	1-6 (454)
X	Genes Dev., Vol. 7, 1993, Patton, J. G. et al. "Cloning and characterization of PSF a novel pre-mRNA splicing factor" p. 393-406	1-6 (706)
X	Nucleic Acids Res., Vol. 16, 1988, Stanford, D. R. et al. "The complete primary structure of the human snRNP E protein" p. 10593-10605	1-6 (711)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 84, 1987, Inoue, C. et al. "Evolutionary conservation of the insulinoma gene rig and its possible function" p. 6659-6662	1-6 (723)
X	J. Immunol., Vol. 144, 1990, Jongstra-Bilen, J. et al. "Human and mouse LSP1 genes code for highly conserved phosphoproteins" p. 1104-1110	1-6 (741)
X	Biochem. J., Vol. 248, 1987, Sakai, I. et al. "The cDNA and protein sequences of human lactate dehydrogenase-B" p. 933-936	1-6 (772)

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochim. Biophys. Acta., Vol. 1089, 1991, Tamura, T. et al. "Molecular cloning and sequence analysis of cDNAs for five major subunits of human proteasomes (multicatalytic proteinase complexes)" p. 95-102	1-6 (775)
X	Mol. Cell. Biol., Vol. 3, 1983, Cowan, N. J. et al. "Expression of human alpha-tubulin genes: interspecies conservation of 3' untranslated regions" p. 1738-1745	1-6 (820)
X	Nucleic Acids Res., Vol. 17, 1989, Taaman, J. W. et al. "Nucleotide sequence of cDNA encoding subunit VIb of human cytochrome c oxidase" p. 1766-1766	1-6 (844)
X	Gene, Vol. 93, 1990 Taanman, J. W., Schrage, C., Ponne, N., Das, A., Bolhuis, P. A., de Vries, H. and Agsteribbe, E. Isolation of cDNAs encoding Subunit VIb of human cytochrome c oxidase and steady-state levels of coxVIb mRNA in different tissues p. 285-291	1-6 (844)
X	J. Biol. Chem., Vol. 264, 1989, Gray, P. W. et al. "Cloning of the cDNA of a human neutrophil bactericidal protein: Structural and functional correlations" p. 9505-9509	1-6 (861)
X	Immunogenetics, Vol. 32, 1990, Angelisova, P. et al. "The human leucocyte surface antigen CD53 is a protein structurally similar to the CD37 and MRC OX-44 antigens" p. 281-285	1-6 (1158)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Koken, M. H. et al. "Structural and functional conservation of two human homologs of the yeast DNA repair gene RAD6" p. 8865-8869	1-6 (1181)
X	Oncogene, Vol. 5, 1990, Firnbach-Kraft, I. et al. "Tyk 2, prototype of a novel class of non-receptor tyrosine Kinase genes" p. 1329-1336	1-6 (1345)
X	Science, Vol. 248, 1990, Smith, C. A. et al. "A receptor for human tumor necrosis factor defines an unusual family of cellular and viral proteins" p. 1019-1023	1-6 (1431)

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 263, 1988, Luster, A. D. et al. "Molecular and biochemical characterization of a novel gamma-interferon-inducible protein" p. 12036-12043	1-6 (1455)
X	J. Clin. Invest., Vol. 83, 1989, Look, A. T. et al. "The human myeloid plasma membrane glycoprotein CD13 (gp150) is identical to aminopeptidase N" p. 1299-1307	1-6 (1469)
X	J. Cell Biol., Vol. 105, 1987, Argraves, W. S. et al. "Amino Acid Sequence of the Human Fibronectin Receptor" p. 1183-1190	1-6 (1607)
X	Nucleic Acids Res., Vol. 18, 1990, Liebhaver, S. A. et al. "Characterization of a human cDNA encoding a widely expressed and highly conserved cysteine-rich protein with an unusual zinc-finger motif" p. 3871-3879	1-6 (1642)
X	J. Biol. Chem., Vol. 264, 1989, Didsbury, J. et al. "Rac, a novel ras-related family of proteins that are bolulinum toxin substrates" p. 16378-16382	1-6 (1709)
X	EMBO J., Vol. 6, 1987, Willison, K. et al. "The human homologue of the mouse t-complex gene, TCP1, is located on chromosome 6 but is not near the HLA region" p. 1967-1974	1-6 (1749)
X	J. Biol. Chem., Vol. 266, 1991, Wu, Y. et al. "Activation of globin gene expression by cDNAs from induced K562 cells: Evidence for involvement of ferritin in globin gene expression" p. 17566-17572	1-6 (1785)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ikuta, T. et al. "Three human alcohol dehydrogenase subunits: cDNA structure and molecular and evolutionary divergence" p. 634-638	1-6 (1864)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Fukumoto, H. et al. "Sequence, tissue distribution, and chromosomal localization of mRNA encoding a human glucose transporter-like protein" p. 5434-5438	1-6 (1878)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Clin. Invest., Vol. 76, 1985, Cooke, N.E. et al. "Serum vitamin D-binding protein is a third member of the albumin and alpha fetoprotein gene family" p. 2420-2424	1-6 (1888)
X	J. Biol. Chem., Vol. 264, 1989, Huang, S.-H. et al. "Human deoxycytidine kinase: Sequence of cDNA clones and analysis of expression in cell lines with and without enzyme activity" p. 14762-14768	1-6 (1894)
X	J. Biol. Chem., Vol. 266, 1991, Huang, S.-H. et al. "Additions and corrections Human deoxytidine kinase. Sequence of cDNA clones and analysis of expression in cell lines with and without anzyme activity" p. 5353-5353	1-6 (1894)
X	Somat. Cell Mol. Genet., Vol. 11, 1985, Bell, G.I. et al. "Human alpha-2-macroglobulin gene is located on chromosome 12" p. 285-289	1-6 (1895)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 81, 1984, Yang, F. et al. "Human transferrin: cDNA characterization and chromosomal localization" p. 2752-2756	1-6 (1902)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 83, 1986, Ny, T. et al. "Cloning and sequence of a cDNA coding for the human beta-migrating endothelial-cell-type plasminogen activator inhibitor" p. 6776-6780	1-6 (1904)
X	J. Biol. Chem., Vol. 267, 1992, Bausch-Jurken, M. T. et al. "Molecular cloning of AMP deaminase isoform L: Sequence and bacterial expression of human AMPD2 cDNA" p. 22407-22413	1-6 (1908)
X	Gene, Vol. 44, 1986, Board, P. G. et al. "Molecular cloning and nucleotide sequence of human alpha-1 acid glycoprotein cDNA" p. 127-131	1-6 (1921)
X	Eur. J. Biochem., Vol. 155, 1986, Wathelet, M. et al. "Molecular cloning, full-length sequence and preliminary characterization of a 56-kDa protein induced by human interferons" p. 11-17	1-6 (2101)

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INTERNATIONAL SEARCH REPORT

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Nucleic Acids Res., Vol. 11, 1983, Chebath, J. et al. "Interferon induced 56,000 mr protein and its mRNA in human cells: molecular cloning and partial sequence of the cDNA" p. 1213-1226	1-6 (2101)
X	Biochemistry, Vol. 25, 1986, Koide, T. et al. "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA" p. 2220-2225	1-6 (2174)
X	Biochemistry, Vol. 22, 1983, Friezner-Degen, S. J. et al. "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin" p. 2087-2097	1-6 (2214)
X	Biochem. J., Vol. 268, 1990, Steinkasserer, A. et al. "Heterogeneity in human serum amyloid A protein. Five different variants from one individual demonstrated by cDNA sequence analysis." p. 287-193	1-6 (2238)
X	Nucleic Acids Res., Vol. 17, 1989, Fabrizi, G. M. et al. "Sequence of a cDNA specifying subunit VIIa of human cytochrome c oxidase" p. 7107-7107	1-6 (2264)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 86, 1989, Sims, J. E. et al. "Cloning of the interleukin 1 receptor from human T cells" p. 8946-8950	1-6 (2265)
X	Eur. J. Biochem., Vol. 169, 1987, Mackinnon, C. M. et al. "Molecular cloning of cDNA for human complement component C1s. The complete amino acid sequence" p. 547-553	1-6 (2266)
X	J. Virol., Vol. 65, 1990, Tsujimoto, A. et al. "Isolation of cDNA for DNA binding proteins which specifically bind to TAX-responsive enhancer element in the LTR of HTLA-1" p. 1420-1426	1-6 (2475)
X	Immunogenetics, Vol. 37, 1993, Emi, N. et al. "Isolation of a novel cDNA clone showing marked similarity to ME491/CD63 superfamily" p. 193-198	1-6 (2556)
X	Nature, Vol. 353, 1991, Kelly, A. P. et al. "A new human HLA class II-related locus, DM" p. 571-573	1-6 (2583)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Hla, T. et al. "An abundant transcript induced in differentiating human endothelial cells encodes a polypeptide with structural similarities to G-protein-coupled receptors" p. 9308-9313	1-6 (2600)
X	J. Biol. Chem., Vol. 267, 1992, White, R. T. et al. "Human adipsin is identical to complement factor D and expressed at high levels in adipose tissue" p. 9210-9213	1-6 (2802)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Rouault, T. A. et al. "Cloning of the cDNA encoding RNA regulatory protein-the human iron-responsive element-binding protein" p. 7958-7962	1-6 (2832)
X	Nucleic Acids Res., Vol. 17, 1989, Sawada, R. et al. "Complementary DNA sequence and deduced peptide sequence for CD59/MEM43 antigen, the human homologue of murine lymphocyte antigen Ly-6c" p. 6728-6728	1-6 (2954)
X	DNA Cell Biol., Vol. 9, 1990, Sawada, R. et al. "Isolation and expression of the full-length cDNA encoding CD59 antigen of human lymphocytes" p. 213-220	1-6 (2954)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 87, 1990, Weller, P. A. et al. "Complete sequence of human vinculin and assignment of the gene to chromosome 10" p. 5667-5671	1-6 (2983)
X	Cell, Vol. 58, 1989, Mellentin, J. D. et al. "LYL-1, a novel gene involved by chromosomal translocation in T-cell leukemia, codes for a protein with a helix-loop-helix DNA binding motif" p. 77-83	1-6 (3023)
X	Cell, Vol. 60, 1990, Uze, G. et al. "Genetic transfer of a functional human interferon alpha receptor into mouse cells: Cloning and expression of its cDNA" p. 225-234	1-6 (3041)
X	Biochem. Biophys. Res. Commun., Vol. 179, 1991, Xiao, L. et al. "Characterization of a full length cDNA which codes for the human spermidine/spermine N-1-acetyltransferase" p. 407-415	1-6 (3053)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 266, 1991, Casero, R. A. Jr. et al. "Isolation and characterization of a cDNA clone that codes for human spermidine/spermine N-1-acetyltransferase" p. 810-814	1-6 (3053)
X	Nucleic Acids Res., Vol. 20, 1992, Wintzerith, M. et al. "Sequence of the human RNA polymerase II largest subunit" p. 910-910	1-6 (3083)
X	J. Cell Biol., Vol. 103, 1986, Lawler, J. et al. "The Structure of Human Thrombospondin, an/ adhesive Glycoprotein with Multiple Calcium binding Sites and Homologies with Several Different Proteins" p. 1635-1648	1-6 (3266)
X	Nature, Vol. 352, 1991, Maslen, C. L. et al. "Partial sequence of a candidate gene for the marfan syndrome" p. 334-337	1-6 (3334)
X	J. Cell Biol., Vol. 111, 1990, Fishman, G. I. et al. "Molecular Characterization and Functional Expression of the Human Cardiac Gap Junction Channel" p. 589-598	1-6 (3403)
X	Cell, Vol. 40, 1985, Ebina, Y. et al. "The human insulin receptor cDNA: The structural basis for hormone-activated membrane signalling" p. 747-758	1-6 (3447)
X	Oncogene, Vol. 5, 1990, Westin, E. H. et al. "Alternative splicing of the human c-myb gene" p. 1117-1124	1-6 (3529)
X	Genomics, Vol. 4, 1989, Todd, S. et al. "cDNA sequence, interspecies comparison and gene mapping analysis of argininosuccinate lyase" p. 53-59	1-6 (3575)
X	FEBS Lett., Vol. 207, 1986, Codina, J. et al. "-Subunits of the human liver Gs/Gi signal-transducing proteins and those of bovine retinal rod cell transducin are identical" p. 187-192	1-6 (3796)
X	Nucleic Acids Res., Vol. 18, 1990, Roessler, B. J. et al. "Cloning of two distinct copies of human phosphoribosyl pyrophosphate synthetase cDNA" p. 193-193	1-6 (3828)

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biochem., Vol. 109, 1991, Sonoda, T. et al. "Complete nucleotide sequence of human phosphoribosyl pyrophosphate synthetase subunit I (PRS I) cDNA and a comparison with human and rat PRPS gene families" p. 361-364	1-6 (3828)
X	J. Biol. Chem., Vol. 263, 1988, Wermuth, B. et al. "Human carbonyl reductase: Nucleotide sequence analysis of a cDNA and amino acid sequence of the encoded protein" p. 16185-16188	1-6 (4033)
X	Biochim. Biophys. Acta. Vol. 1048, 1990, Forrest, G. L. et al. "Induction of a human carbonyl reductase gene located on chromosome 21" p. 149-155	1-6 (4033)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 88, 1991, Schuetz, T. J. et al. "Isolation of a cDNA for HSF2: Evidence for two heat shock factor genes in humans" p. 6911-6915	1-6 (4093)
X	Nucleic Acids Res., Vol. 13, 1985, Hallewell, R. A. et al. "Human Cu/Zn superoxide dismutase cDNA: isolation of clones synthesising high levels of active or inactive enzyme from an expression library" p. 2017-2034	1-6 (4110)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 80, 1983, Sherman, L. et al. "Nucleotide sequence and expression of human chromosome 21 - encoded superoxide dismutase mRNA" p. 5465-5469	1-6 (4110)
X	J. Biol. Chem., Vol. 268, 1993, David, V. et al. "Interaction with newly synthesized and retained proteins in the endoplasmic reticulum suggests a chaperone function for human integral membrane protein IP90 (calnexin)" p. 9585-9592	1-6 (4373)
X	J. Exp. Med., Vol. 172, 1990, Tekamp-Olson, P. et al. "Cloning and Characterization of cDNAs for Murine Macrophage Inflammatory Protein 2 and its Human Homologues" p. 911-919	1-6 (4452)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Biochemistry, Vol. 30, 1991, Tomkinson, B. et al. "Characterization of cDNA for human tripeptidyl peptidase II: The N-terminal part of the enzyme is similar to subtilisin" p. 168-174	1-6 (4522)
X	J. Biol. Chem., Vol. 263, 1988, Verma, A. K. et al. "Complete primary structure of a human plasma membrane Ca ²⁺ pump" p. 14152-14159	1-6 (4673)
X	J. Biol. Chem., Vol. 267, 1992, Shechter, I. et al. "Solubilization, purification and characterization of a truncated form of rat hepatic squalene synthetase" p. 8628-8635	1-6 (4818)
X	J. Biol. Chem., Vol. 267, 1992, McKenzie, T. L. et al. "Molecular cloning, expression, and characterization of the cDNA for the rat hepatic squalene synthase" p. 21368-21374	1-6 (4818)
X	Nucleic Acids Res., Vol. 13, 1985, Furutani, Y. et al. "Cloning and characterization of the cDNAs for human and rabbit interleukin-1 precursor" p. 5869-5882	1-6 (4872)
X	Proc. Natl. Acad. Sci U.S.A., Vol. 89, 1992, Katoh, M. et al. "K-sam gene encodes secreted as well as transmembrane receptor tyrosine kinase" p. 2960-2964	1-6 (4914)
X	Differentiation, Vol. 42, 1989, Kuruc, N. et al. "Synthesis of cytokeratin 13, a component characteristic of internal stratified epithelia, is not induced in human epidermal tumors" p. 111-123	1-6 (5264)
X	J. Biol. Chem., Vol. 266, 1991, Kiefer, M. C. et al. "Identification and molecular cloning of two new 30-kDa insulin-like growth factor binding proteins isolated from adult human serum" p. 9043-9049	1-6 (5374)

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International application No.

PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^o	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	J. Biol. Chem., Vol. 265, 1990, Opipari, A. W. et al. "The A20 cDNA induced by tumor necrosis factor alpha-encodes a novel type of zinc finger protein" p. 14705-14708	1-6 (5427)
X	J. Biol. Chem., Vol. 265, 1990, McLean, J. W. et al. "cDNA sequence of the human integrin beta-5 subunit" p. 17126-17131	1-6 (5715)
X	Cell, Vol. 66, 1991, Ge, H. et al. "primary structure of the human splicing factor ASF reveals similarities with drosophila regulators" p. 373-382	1-6 (5860)
X	Cancer Res., Vol. 52, 1992, Kondoh, N. et al. "Differential expression of S19 ribosomal protein, laminin binding protein and HLA class I mRNAs associated with colon carcinoma progression and differentiation" p. 791-796	1-6 (6439)
X	J. Biol. Chem., Vol. 263, 1988, Collart, F. R. et al. "Cloning and sequence analysis of the human and chinese hamster inosine-5' -monophosphate dehydrogenase cDNA" p. 15769-15772	1-6 (6471)
X	J. Biol. Chem., Vol. 261, 1986, Romeo, P. -H. et al. "Molecular cloning and nucleotide sequence of a complete human uroporphyrinogen decarboxylase cDNA" p. 9825-9831	1-6 (6569)
X	J. Cell Biol., Vol. 106, 1988, Leube, R. E. et al. "Molecular characterization and expression of the stratification-related cytokeratins 4 and 15" p. 1249-1261	1-6 (6875)
X	Proc. Natl. Acad. Sci. U.S.A., Vol. 85, 1988, Daher, K. A. et al. "Isolation and characterization of human defensin cDNA clones" p. 7327-7331	1-6 (7106)
X	J. Exp. Med, Vol. 172, 1990, Larsen, A. et al. "Expression Cloning of a Human Graulocyte Colony-stimulating Factor Receptor: a Structural Mosaic of Hematopoietin Receptor, Immunoglobulin, and Fibronectin Domains" p. 1559-1570	1-6 (7126)

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PCT/JP94/01916

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category ^a	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Oncogene, Vol. 8, 1993, Schulz, A. S. et al. "The genomic structure of the human UFO receptor" p. 509-513	1-6 (7790)
A	Nature Genetics, Vol. 2, 1992, Okubo, K. et al. "Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression" p. 173-179	1-6
A	Nature Genetics, Vol. 2, 1992, Khan, A. S. et al. "Single pass sequencing and physical and genetic mapping of human brain cDNAs" p. 180-188	1-6